

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys	Gly	Asn	Leu	Thr	Gly	Asn	Ser	Lys	Lys	Ala	Ala	Asp	Ser	Gly	Asp	1	5	10	15
Lys	Pro	Val	Ile	Lys	Met	Tyr	Gln	Ile	Gly	Asp	Lys	Pro	Asp	Asn	Leu	20	25	30	
Asp	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Lys	Ile	Ile	Glu	Glu	Lys	Val	Gly	35	40	45	
Ala	Lys	Leu	Asp	Ile	Gln	Tyr	Leu	Gly	Trp	Gly	Asp	Tyr	Gly	Lys	Lys	50	55	60	
Met	Ser	Val	Ile	Thr	Ser	Ser	Gly	Glu	Asn	Tyr	Asp	Ile	Ala	Phe	Ala	65	70	75	80
Asp	Asn	Tyr	Ile	Val	Asn	Ala	Gln	Lys	Gly	Ala	Tyr	Ala	Asp	Leu	Thr	85	90	95	
Glu	Leu	Tyr	Lys	Lys	Glu	Gly	Lys	Asp	Leu	Tyr	Lys	Ala	Leu	Asp	Pro	100	105	110	
Ala	Tyr	Ile	Lys	Gly	Asn	Thr	Val	Asn	Gly	Lys	Ile	Tyr	Ala	Val	Pro	115	120	125	
Val	Ala	Ala	Asn	Val	Ala	Ser	Gln	Asn	Phe	Ala	Phe	Asn	Gly	Thr	130	135	140		
Leu	Leu	Ala	Lys	Tyr	Gly	Ile	Asp	Ile	Ser	Gly	Val	Thr	Ser	Tyr	Glu	145	150	155	160
Thr	Leu	Glu	Pro	Val	Leu	Lys	Gln	Ile	Lys	Glu	Lys	Ala	Pro	Asp	Val	165	170	175	
Val	Pro	Phe	Ala	Ile	Gly	Lys	Val	Phe	Ile	Pro	Ser	Asp	Asn	Phe	Asp	180	185	190	
Tyr	Pro	Val	Ala	Asn	Gly	Leu	Pro	Phe	Val	Ile	Asp	Leu	Glu	Gly	Asp	195	200	205	
Thr	Thr	Lys	Val	Val	Asn	Arg	Tyr	Glu	Val	Pro	Arg	Phe	Lys	Glu	His	210	215	220	
Leu	Lys	Thr	Leu	His	Lys	Phe	Tyr	Glu	Ala	Gly	Tyr	Ile	Pro	Lys	Asp	225	230	235	240
Val	Ala	Thr	Ser	Asp	Thr	Ser	Phe	Asp	Leu	Gln	Gln	Asp	Thr	Trp	Phe	245	250	255	
Val	Arg	Glu	Glu	Thr	Val	Gly	Pro	Ala	Asp	Tyr	Gly	Asn	Ser	Leu	Leu	260	265	270	
Ser	Arg	Val	Ala	Asn	Lys	Asp	Ile	Gln	Ile	Lys	Pro	Ile	Thr	Asn	Phe	275	280	285	
Ile	Lys	Xaa	Asn	Gln	Thr	Thr	Gln	Val	Ala	Asn	Phe	Val	Ile	Ser	Asn	290	295	300	
Asn	Ser	Lys	Asn	Lys	Glu	Lys	Ser	Met	Glu	Ile	Leu	Asn	Leu	Leu	Asn	305	310	315	320
Thr	Asn	Pro	Glu	Leu	Leu	Asn	Gly	Leu	Val	Tyr	Gly	Pro	Glu	Gly	Lys				

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325

330

335

Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp  
 340 345 350

Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn  
 355 360 365

Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn  
 370 375 380

Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe  
 385 390 395 400

Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn  
 405 410 415

Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro  
 420 425 430

Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala  
 435 440 445

Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu  
 450 455 460

Lys Asn Lys Lys  
 465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTGGTATATC AACGGAAAGG CACCATTTGC AGTGTATTTT CAAGACTACA TGGCTAAGAA	240
ATTGGAAAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGGTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAACTTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAAC TCAACCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

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TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780  
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840  
 CGCAGCTCGC TGGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900  
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys	1	5	10	15
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu	20	25	30	
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val	35	40	45	
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn	50	55	60	
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys	65	70	75	80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His	85	90	95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro	100	105	110	
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu	115	120	125	
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu	130	135	140	
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile	145	150	155	160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly	165	170	175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys	180	185	190	
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn	195	200	205	
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln	210	215	220	

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Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala  
 225 230 235 240

Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp  
 245 250 255

Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp  
 260 265 270

Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr  
 275 280 285

Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys  
 290 295 300

Gly Phe Thr Asn Glu Phe Val Lys  
 305 310

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT	60
CGATGAAATC AAAAAAAGCG GTGAACTGCG AATCGCCGTG TTTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTTAA ATACATTTCA GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTCGTATC	360
ACCTAAGACT GGTCTCATTA CAGACGTCAA ACAACTTGAA GGTAAAACCT TAATTGTCAC	420
AAAAGGA 3 ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTGA CTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC	540
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAAT AAAGGATTTG AAGTAGGAAT	600
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAAACTTCT TCCACAAGGC	720
CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Ser Ser Gly Gly Asn Ala Gly Ser Ser Ser Gly Lys Thr Thr Ala Lys
1           5           10           15
Ala Arg Thr Ile Asp Glu Ile Lys Lys Ser Gly Glu Leu Arg Ile Ala
20           25           30
Val Phe Gly Asp Lys Lys Pro Phe Gly Tyr Val Asp Asn Asp Gly Ser
35           40           45
Thr Lys Val Arg Tyr Asp Ile Glu Leu Gly Asn Gln Leu Ala Gln Asp
50           55           60
Leu Gly Val Lys Val Lys Tyr Ile Ser Val Asp Ala Ala Asn Arg Ala
65           70           75           80
Glu Tyr Leu Ile Ser Asn Lys Val Asp Ile Thr Leu Ala Asn Phe Thr
85           90           95
Val Thr Asp Glu Arg Lys Lys Gln Val Asp Phe Ala Leu Pro Tyr Met
100          105          110
Lys Val Ser Leu Gly Val Val Ser Pro Lys Thr Gly Leu Ile Thr Asp
115          120          125
Val Lys Gln Leu Glu Gly Lys Thr Leu Ile Val Thr Lys Gly Thr Thr
130          135          140
Ala Glu Thr Tyr Phe Glu Lys Asn His Pro Glu Ile Lys Leu Gln Lys
145          150          155          160
Tyr Asp Gln Tyr Ser Asp Ser Tyr Gln Ala Leu Leu Asp Gly Arg Gly
165          170          175
Asp Ala Phe Ser Thr Asp Asn Thr Glu Val Leu Ala Trp Ala Leu Glu
180          185          190
Asn Lys Gly Phe Glu Val Gly Ile Thr Ser Leu Gly Asp Pro Asp Thr
195          200          205
Ile Ala Ala Ala Val Gln Lys Gly Asn Gln Glu Leu Leu Asp Phe Ile
210          215          220
Asn Lys Asp Ile Glu Lys Leu Gly Lys Glu Asn Phe Phe His Lys Ala
225          230          235          240
Tyr Glu Lys Thr Leu His Pro Thr Tyr Gly Asp Ala Ala Lys Ala Asp
245          250          255
Asp Leu Val Val Glu Gly Gly Lys Val Asp
260          265

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

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(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAACATAT GGTAAATCTG CGGATGGCAC AGTGACCATC GAGTATTTCA ACCAGAAAAA	60
AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT	120
CAAGGTCAAA GTCGTCAATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCGTTCTCGC	180
AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC	240
AAAAGCAGGT GTTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG	300
CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC	360
TTATGGAATT TACTACAACA AAGATAAATT CGAAGAAGT GGCCTGAAGG TTCCTGAAAC	420
CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAAGGACAAA CACCATTTGG	480
AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCGACAGC	540
AACAGGTGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA	600
ATTGTCGGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG	660
ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG	720
TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA	780
ACCGAACTTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAAGGAC AAAGCTTAAC	840
CGTTGGTGCG GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC	900
CAATGCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAAATACT ACGATGTGGA	960
CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTCAC CGCTTGCTGG	1020
TATGACCGAA TATGCCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG	1080
TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT	1140
GGTCAATGAT TTGAATGCCT TCTTTAACCC GATGAAAGCG GATGTGGAT	1189

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5					10					15	

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Asn	Gln	Lys	Lys	Glu	Met	Thr	Lys	Thr	Leu	Glu	Glu	Ile	Thr	Arg	Asp		
			20					25						30			
Phe	Glu	Lys	Glu	Asn	Pro	Lys	Ile	Lys	Val	Lys	Val	Val	Asn	Val	Pro		
		35					40						45				
Asn	Ala	Gly	Glu	Val	Leu	Lys	Thr	Arg	Val	Leu	Ala	Gly	Asp	Val	Pro		
	50					55					60						
Asp	Val	Val	Asn	Ile	Tyr	Pro	Gln	Ser	Ile	Glu	Leu	Gln	Glu	Trp	Ala		
65					70					75					80		
Lys	Ala	Gly	Val	Phe	Glu	Asp	Leu	Ser	Asn	Lys	Asp	Tyr	Leu	Lys	Arg		
				85					90					95			
Val	Lys	Asn	Gly	Tyr	Ala	Glu	Lys	Tyr	Ala	Val	Asn	Glu	Lys	Val	Tyr		
			100					105					110				
Asn	Val	Pro	Phe	Thr	Ala	Asn	Ala	Tyr	Gly	Ile	Tyr	Tyr	Asn	Lys	Asp		
		115					120						125				
Lys	Phe	Glu	Glu	Leu	Gly	Leu	Lys	Val	Pro	Glu	Thr	Trp	Asp	Glu	Phe		
	130					135					140						
Glu	Gln	Leu	Val	Lys	Asp	Ile	Val	Ala	Lys	Gly	Gln	Thr	Pro	Phe	Gly		
145					150					155					160		
Ile	Ala	Gly	Ala	Asp	Ala	Trp	Thr	Leu	Asn	Gly	Tyr	Asn	Gln	Leu	Ala		
				165					170					175			
Phe	Ala	Thr	Ala	Thr	Gly	Gly	Gly	Lys	Glu	Ala	Asn	Gln	Tyr	Leu	Arg		
			180					185					190				
Tyr	Ser	Gln	Pro	Asn	Ala	Ile	Lys	Leu	Ser	Asp	Pro	Ile	Met	Lys	Asp		
		195					200					205					
Asp	Ile	Lys	Val	Met	Asp	Ile	Leu	Arg	Ile	Asn	Gly	Ser	Lys	Gln	Lys		
	210					215					220						
Asn	Trp	Glu	Gly	Ala	Gly	Tyr	Thr	Asp	Val	Ile	Gly	Ala	Phe	Ala	Arg		
225					230					235					240		
Gly	Asp	Val	Leu	Met	Thr	Pro	Asn	Gly	Ser	Trp	Ala	Ile	Thr	Ala	Ile		
				245					250					255			
Asn	Glu	Gln	Lys	Pro	Asn	Phe	Lys	Ile	Gly	Thr	Phe	Met	Ile	Pro	Gly		
			260					265					270				
Lys	Glu	Lys	Gly	Gln	Ser	Leu	Thr	Val	Gly	Ala	Gly	Asp	Leu	Ala	Trp		
		275					280					285					
Ser	Ile	Ser	Ala	Thr	Thr	Lys	His	Pro	Lys	Glu	Ala	Asn	Ala	Phe	Val		
	290					295					300						
Glu	Tyr	Met	Thr	Arg	Pro	Glu	Val	Met	Gln	Lys	Tyr	Tyr	Asp	Val	Asp		
305					310					315					320		
Gly	Ser	Pro	Thr	Ala	Ile	Glu	Gly	Val	Lys	Gln	Ala	Gly	Glu	Asp	Ser		
				325					330					335			
Pro	Leu	Ala	Gly	Met	Thr	Glu	Tyr	Ala	Phe	Thr	Asp	Arg	His	Leu	Val		
			340					345					350				

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Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp  
385 390 395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGGGAAAAAT	TCTAGCGAAA	CTAGTGGAGA	TAATTGGTCA	AAGTACCAGT	CTAACAAGTC	60
TATTACTATT	GGATTTGATA	GTACTTTTGT	TCCAATGGGA	TTTGCTCAGA	AAGATGGTTC	120
TTATGCAGGA	TTTGATATTG	ATTTAGCTAC	AGCTGTTTTT	GAAAAATACG	GAATCACGGT	180
AAATTGGCAA	CCGATTGATT	GGGATTTGAA	AGAAGCTGAA	TTGACAAAAG	GAACGATTGA	240
TCTGATTTGG	AATGGCTATT	CCGCTACAGA	CGAACGCCGT	GAAAAGGTGG	CTTTCAGTAA	300
CTCATATATG	AAGAATGAGC	AGGTATTGGT	TACGAAGAAA	TCATCTGGTA	TCACGACTGC	360
AAAGGATATG	ACTGGAAAGA	CATTAGGAGC	TCAAGCTGGT	TCATCTGGTT	ATGCGGACTT	420
TGAAGCAAAT	CCAGAAATTT	TGAAGAATAT	TGTCGCTAAT	AAGGAAGCGA	ATCAATACCA	480
AACCTTTAAT	GAAGCCTTGA	TTGATTTGAA	AAACGATCGA	ATTGATGGTC	TATTGATTGA	540
CCGTGTCTAT	GCAAAC TATT	ATTTAGAAGC	AGAAGGTGTT	TTAAACGATT	ATAATGTCTT	600
TACAGTTGGA	CTAGAAACAG	AAGCTTTTGC	GGTTGGAGCC	CGTAAGGAAG	ATACAAACTT	660
GGTTAAGAAG	ATAAATGAAG	CTTTTCTAG	TCTTTACAAG	GACGGCAAGT	TCCAAGAAAT	720
CAGCCAAAAA	TGGTTTGGAG	AAGATGTAGC	AACCAAAGAA	GTAAAAAGAAG	GACAG	775

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met

131

20

25

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Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu  
35 40 45

Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro  
50 55 60

Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp  
65 70 75 80

Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val  
85 90 95

Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys  
100 105 110

Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu  
115 120 125

Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro  
130 135 140

Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln  
145 150 155 160

Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly  
165 170 175

Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly  
180 185 190

Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala  
195 200 205

Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile  
210 215 220

Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile  
225 230 235 240

Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu  
245 250 255

Gly Gln

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAACTC	60
AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT	120

TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180  
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT 240  
 TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300  
 CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360  
 TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420  
 CAAAGACCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480  
 AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540  
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600  
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT 660  
 TGAAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720  
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780  
 CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840  
 TGACAAGATT GCTGAAGGAT TGGCAAAA 868

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val  
 1 5 10 15  
 Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp  
 20 25 30  
 Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu  
 35 40 45  
 Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu  
 50 55 60  
 Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe  
 65 70 75 80  
 Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe  
 85 90 95  
 Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu  
 100 105 110  
 Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile  
 115 120 125

Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn  
 130 135 140  
 Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu  
 145 150 155 160  
 Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala  
 165 170 175  
 Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser  
 180 185 190  
 Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu  
 195 200 205  
 Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg  
 210 215 220  
 Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg  
 225 230 235 240  
 Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln  
 245 250 255  
 Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr  
 260 265 270  
 Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala  
 275 280 285  
 Lys

## (2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1546 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCCT	60
TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC	120
AAATGAAAAG TTAATTTTGC AACGTTTGGA GAAGGAAACT GCGTTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG	300
TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTCA ACGATATGGC	480
TTGGATTAAC AAAGATTGGC TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTACTGATGA	540

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA 600  
 TGAAATTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC 660  
 TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA 720  
 CTTACACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA 780  
 AAAAGGCCTG ATTGATAAAG AAGCTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG 840  
 TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA 900  
 CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG 960  
 TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT 1020  
 AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA 1080  
 CTGGGGAAC TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA 1140  
 TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA 1200  
 AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA 1260  
 TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320  
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA 1380  
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440  
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT 1500  
 CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val  
 1 5 10 15

Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser  
 20 25 30

Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg  
 35 40 45

Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser  
 50 55 60

Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro  
 65 70 75 80

Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

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85								90					95				
Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val	Glu	Asp	Leu	Ile	Asp	Lys	Tyr		
			100					105						110			
Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp	Glu	Lys	Pro	Glu	Tyr	Lys	Ala		
			115					120						125			
Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile	Tyr	Ser	Phe	Pro	Trp	Ile	Glu		
			130					135						140			
Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile	His	Ser	Val	Asn	Asp	Met	Ala		
			145					150						155			
Trp	Ile	Asn	Lys	Asp	Trp	Leu	Lys	Lys	Leu	Gly	Leu	Glu	Met	Pro	Lys		
			165					170						175			
Thr	Thr	Asp	Asp	Leu	Ile	Lys	Val	Leu	Glu	Ala	Phe	Lys	Asn	Gly	Asp		
			180					185						190			
Pro	Asn	Gly	Asn	Gly	Glu	Ala	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ile	Ser		
			195					200						205			
Gly	Asn	Gly	Asn	Glu	Asp	Phe	Lys	Phe	Leu	Phe	Ala	Ala	Phe	Gly	Ile		
			210					215						220			
Gly	Asp	Asn	Asp	Asp	His	Leu	Val	Val	Gly	Asn	Asp	Gly	Lys	Val	Asp		
			225					230						235			
Phe	Thr	Ala	Asp	Asn	Asp	Asn	Tyr	Lys	Glu	Gly	Val	Lys	Phe	Ile	Arg		
			245					250						255			
Gln	Leu	Gln	Glu	Lys	Gly	Leu	Ile	Asp	Lys	Glu	Ala	Phe	Glu	His	Asp		
			260					265						270			
Trp	Asn	Ser	Tyr	Ile	Ala	Lys	Gly	His	Asp	Gln	Lys	Phe	Gly	Val	Tyr		
			275					280						285			
Phe	Thr	Trp	Asp	Lys	Asn	Asn	Val	Thr	Gly	Ser	Asn	Glu	Ser	Tyr	Asp		
			290					295						300			
Val	Leu	Pro	Val	Leu	Ala	Gly	Pro	Ser	Gly	Gln	Lys	His	Val	Ala	Arg		
			305					310						315			
Thr	Asn	Gly	Met	Gly	Phe	Ala	Arg	Asp	Lys	Met	Val	Ile	Thr	Ser	Val		
			325					330						335			
Asn	Lys	Asn	Leu	Glu	Leu	Thr	Ala	Lys	Trp	Ile	Asp	Ala	Gln	Tyr	Ala		
			340					345						350			
Pro	Leu	Gln	Ser	Val	Gln	Asn	Asn	Trp	Gly	Thr	Tyr	Gly	Asp	Asp	Lys		
			355					360						365			
Gln	Gln	Asn	Ile	Phe	Glu	Leu	Asp	Gln	Ala	Ser	Asn	Ser	Leu	Lys	His		
			370					375						380			
Leu	Pro	Leu	Asn	Gly	Thr	Ala	Pro	Ala	Glu	Leu	Arg	Gln	Lys	Thr	Glu		
			385					390						395			
Val	Gly	Gly	Pro	Leu	Ala	Ile	Leu	Asp	Ser	Tyr	Tyr	Gly	Lys	Val	Thr		
			405					410						415			
Thr	Met	Pro	Asp	Asp	Ala	Lys	Trp	Arg	Leu	Asp	Leu	Ile	Lys	Glu	Tyr		

420

425

430

Tyr Val Pro Tyr Met Ser Asn Val Asn Asn Tyr Pro Arg Val Phe Met  
435 440 445

Thr Gln Glu Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn  
450 455 460

Asp Tyr Ile Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile  
465 470 475 480

Asp Thr Glu Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu  
485 490 495

Ser Asp Tyr Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala  
500 505 510

Asn Lys Asn  
515

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAAAGT TCACTGGACG AGGTCAAACCT TTCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCTTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA	895

(2) INFORMATION FOR SEQ ID NO:24:

096527 0430  
10210 225960

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro
1          5          10          15

Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys
          20          25          30

Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile
          35          40          45

Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr
          50          55          60

Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly
          65          70          75          80

Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp
          85          90          95

Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys
          100          105          110

Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp
          115          120          125

Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu
          130          135          140

Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser
          145          150          155          160

Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu
          165          170          175

Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser
          180          185          190

Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr
          195          200          205

Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val
          210          215          220

Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala
          225          230          235          240

Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu
          245          250          255

Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr
          260          265          270

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Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu  
 275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys  
 290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GGC GGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CCAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300
ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA	360
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC	420
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG	480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA	540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT	600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA	660
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA	720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC	780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG	840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA	900
CCTTGTA AAC GGGTTTGCAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA	960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC	1020
AGGTGCTTTC CCAGTCCGTA CTTCAATTTGG AAAACTTTAT GAAGACAAAC GCATGGAAAC	1080
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTTGCTGA	1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC	1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA	1260
A	1261

(2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly
1           5           10           15
Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu
20           25           30
Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala
35           40           45
Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp
50           55           60
Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr
65           70           75           80
Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly
85           90           95
Lys Asn Gly Lys Leu Ala Glu Leu Asn Asp Leu Phe Thr Asp Glu Phe
100          105          110
Val Lys Asp Val Asn Asn Glu Asn Ile Val Gln Ala Ser Lys Ala Gly
115          120          125
Asp Lys Ala Tyr Met Tyr Pro Ile Ser Ser Ala Pro Phe Tyr Met Ala
130          135          140
Met Asn Lys Lys Met Leu Glu Asp Ala Gly Val Ala Asn Leu Val Lys
145          150          155          160
Glu Gly Trp Thr Thr Asp Asp Phe Glu Lys Val Leu Lys Ala Leu Lys
165          170          175
Asp Lys Gly Tyr Thr Pro Gly Ser Leu Phe Ser Ser Gly Gln Gly Gly
180          185          190
Asp Gln Gly Thr Arg Ala Phe Ile Ser Asn Leu Tyr Ser Gly Ser Val
195          200          205
Thr Asp Glu Lys Val Ser Lys Tyr Thr Thr Asp Asp Pro Lys Phe Val
210          215          220
Lys Gly Leu Glu Lys Ala Thr Ser Trp Ile Lys Asp Asn Leu Ile Asn
225          230          235          240
Asn Gly Ser Gln Phe Asp Gly Gly Ala Asp Ile Gln Asn Phe Ala Asn
245          250          255
Gly Gln Thr Ser Tyr Thr Ile Leu Trp Ala Pro Ala Gln Asn Gly Ile
260          265          270

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Gln Ala Lys Leu Leu Glu Ala Ser Lys Val Glu Val Val Glu Val Pro  
 275 280 285  
 Phe Pro Ser Asp Glu Gly Lys Pro Ala Leu Glu Tyr Leu Val Asn Gly  
 290 295 300  
 Phe Ala Val Phe Asn Asn Lys Asp Asp Lys Lys Val Ala Ala Ser Lys  
 305 310 315 320  
 Lys Phe Ile Gln Phe Ile Ala Asp Asp Lys Glu Trp Gly Pro Lys Asp  
 325 330 335  
 Val Val Arg Thr Gly Ala Phe Pro Val Arg Thr Ser Phe Gly Lys Leu  
 340 345 350  
 Tyr Glu Asp Lys Arg Met Glu Thr Ile Ser Gly Trp Thr Gln Tyr Tyr  
 355 360 365  
 Ser Pro Tyr Tyr Asn Thr Ile Asp Gly Phe Ala Glu Met Arg Thr Leu  
 370 375 380  
 Trp Phe Pro Met Leu Gln Ser Val Ser Asn Gly Asp Glu Lys Pro Ala  
 385 390 395 400  
 Asp Ala Leu Lys Ala Phe Thr Glu Lys Ala Asn Glu Thr Ile Lys Lys  
 405 410 415  
 Ala Met Lys Gln  
 420

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAAA ATGAAGATGG AGAAACTAAG ACAGAACAGA CAGCCAAAGC	60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA	120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA	180
CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT	240
CAAACTCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT	300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC	360
AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT	420
TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT	480
GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC	540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC	600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GGCGGAGACT ACGTCGAT	658

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln  
 1 5 10 15  
 Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala  
 20 25 30  
 Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln  
 35 40 45  
 Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser  
 50 55 60  
 Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val  
 65 70 75 80  
 Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His  
 85 90 95  
 Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp  
 100 105 110  
 Tyr Val Asn Gln Asp Gly Lys Ala Ala Asp Arg Tyr Ser Ala Arg  
 115 120 125  
 Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly  
 130 135 140  
 Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu  
 145 150 155 160  
 Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys  
 165 170 175  
 Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val  
 180 185 190  
 Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu  
 195 200 205  
 Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp  
 210 215

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 790 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGAAAA 60  
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGGTTGTGG 120  
GAAATCAACA CTCATTAAAA CCTTGCTCTG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180  
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240  
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300  
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGAAAA GATGACCTTG AAATAATAAA 360  
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420  
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480  
ACTTTTAGAT GAGCCAACTA CTTACTTGA TATCTCATAT CAAATAGAAC TATTAGACCT 540  
CTTGACTGAT CTAAACCAAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA 600  
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660  
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720  
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA 780  
TGTTAECTCT 790

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile  
1 5 10 15  
Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val  
20 25 30  
Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu  
35 40 45  
Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys  
50 55 60  
Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile  
65 70 75 80  
Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu  
85 90 95

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T0229 2259460

Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly  
 100 105 110  
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val  
 115 120 125  
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg  
 130 135 140  
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu  
 145 150 155 160  
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu  
 165 170 175  
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile  
 180 185 190  
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr  
 195 200 205  
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu  
 210 215 220  
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala  
 225 230 235 240  
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile  
 245 250 255  
 Gly Lys His His Val Ser  
 260

## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACCTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG 60  
 CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC 120  
 CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA 180  
 AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG 240  
 AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT 300  
 GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC 360  
 TGTACCGAAT GACGCTACAA ACGAAAGCCG TCGCCTTTAT TTGCTTCAAT CAGCTGGCTT 420  
 GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC 480  
 AAAGAAGTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT 540

TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600  
 ACTTTTCAAA GAACAAGCTG ATGAAAATC AAAACAATGG TACAACATCA TTGTTGCAAA 660  
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720  
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG 780  
 G 781

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr  
 1 5 10 15  
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu  
 20 25 30  
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp  
 35 40 45  
 Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn  
 50 55 60  
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly  
 65 70 75 80  
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu  
 85 90 95  
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp  
 100 105 110  
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu  
 115 120 125  
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp  
 130 135 140  
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro  
 145 150 155 160  
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser  
 165 170 175  
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu  
 180 185 190  
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu  
 195 200 205

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Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu  
 210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His  
 225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp  
 245 250 255

Gln Pro Val Trp  
 260

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAACTAC CAACGTGTCT TGTACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300
AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA	360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA	420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC	480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA	540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTCGCTTTT AGATGTGGGA TGGTGTCTCT	600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG	640

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val  
 1 5 10 15

Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala

146

20

25

30

Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln  
35 40 45

Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu  
50 55 60

Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala  
65 70 75 80

Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu  
85 90 95

Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu  
100 105 110

Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln  
115 120 125

Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys  
130 135 140

Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser  
145 150 155 160

Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser  
165 170 175

Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala  
180 185 190

Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly  
195 200 205

Thr Pro Ser Leu Gln  
210

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC	60
TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTCAAGT	120
TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAACT AAAGCTACGG TTGTAGAAAA	180
ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG	240
TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA	300
ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG	360
CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG	420

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ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480  
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540  
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600  
 CCGTGTAAT GGTAATGGTG AATGGGTAAA C 631

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr  
 1 5 10 15  
 Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly  
 20 25 30  
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu  
 35 40 45  
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp  
 50 55 60  
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly  
 65 70 75 80  
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys  
 85 90 95  
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr  
 100 105 110  
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly  
 115 120 125  
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe  
 130 135 140  
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr  
 145 150 155 160  
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys  
 165 170 175  
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val  
 180 185 190  
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp  
 195 200 205  
 ---Val Asn  
 210

096532 01304  
 102220 225460

## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC	60
AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC	120
AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT	180
AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA	240
AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT	300
TGAAGAAGCT AAGAAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC	360
CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTA AAAAAGC	420
GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA	480
AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC	540
AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA	600
AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC	660
AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA	720
AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA	780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA	840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA	900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA	960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA	1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA	1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA	1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT	1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC	1360

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids

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(ii) MOLECULE TYPE: protein

Asp	Glu	Gln	Lys	Ile	Lys	Gln	Ala	Glu	Ala	Glu	Val	Glu	Ser	Lys	Gln	
1				5					10					15		
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Lys	Ile	Lys	Thr	Asp	Arg	Glu	Glu	Ala	
			20					25					30			
Glu	Glu	Glu	Ala	Lys	Arg	Arg	Ala	Asp	Ala	Lys	Glu	Gln	Gly	Lys	Pro	
		35					40					45				
Lys	Gly	Arg	Ala	Lys	Arg	Gly	Val	Pro	Gly	Glu	Leu	Ala	Thr	Pro	Asp	
	50					55					60					
Lys	Lys	Glu	Asn	Asp	Ala	Lys	Ser	Ser	Asp	Ser	Ser	Val	Gly	Glu	Glu	
65					70					75					80	
Thr	Leu	Pro	Ser	Pro	Ser	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	
				85					90					95		
Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Glu	Asp	Gln	Lys	Glu	
			100					105					110			
Glu	Asp	Arg	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	
		115					120					125				
Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu	Leu	Glu	Leu	
	130					135					140					
Val	Lys	Glu	Glu	Ala	Lys	Glu	Pro	Arg	Asn	Glu	Glu	Lys	Val	Lys	Gln	
145					150					155					160	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Lys	Lys	Ala	Glu	Ala	Thr	Arg	Leu	Glu	
				165					170					175		
Lys	Ile	Lys	Thr	Asp	Arg	Lys	Lys	Ala	Glu	Glu	Glu	Ala	Lys	Arg	Lys	
			180					185					190			
Ala	Ala	Glu	Glu	Asp	Lys	Val	Lys	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Gln	
		195					200					205				
Pro	Ala	Pro	Ala	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Lys	Pro	
	210					215					220					
Glu	Asn	Pro	Ala	Glu	Gln	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Asp	Gln	Gln	
225					230					235					240	
Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	Leu	
				245					250					255		
Thr	Gln	Gln	Gln	Pro	Pro	Lys	Thr	Glu	Lys	Pro	Ala	Gln	Pro	Ser	Thr	
			260					265					270			
Pro	Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	
		275					280					285				

150

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp  
290 295 300

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn  
305 310 315 320

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly  
325 330 335

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser  
340 345 350

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn  
355 360 365

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp  
370 375 380

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp  
385 390 395 400

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser  
405 410 415

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly  
420 425 430

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn  
435 440 445

Gly Glu Trp Val Asn  
450

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids

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- (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys	Gly	Glu	Glu	Glu	Thr	Lys	Lys	Thr	Gln	Ala	Ala	Gln	Gln	Pro	Lys	1	5	10	15
Gln	Gln	Thr	Thr	Val	Gln	Gln	Ile	Ala	Val	Gly	Lys	Asp	Ala	Pro	Asp	20	25	30	
Phe	Thr	Leu	Gln	Ser	Met	Asp	Gly	Lys	Glu	Val	Lys	Leu	Ser	Asp	Phe	35	40	45	
Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp	Cys	Gly	Pro	50	55	60	
Cys	Lys	Lys	Ser	Met	Pro	Glu	Leu	Met	Glu	Leu	Ala	Ala	Lys	Pro	Asp	65	70	75	80
Arg	Asp	Phe	Glu	Ile	Leu	Thr	Val	Ile	Ala	Pro	Gly	Ile	Gln	Gly	Glu	85	90	95	
Lys	Thr	Val	Glu	Gln	Phe	Pro	Gln	Trp	Phe	Gln	Glu	Gln	Gly	Tyr	Lys	100	105	110	
Asp	Ile	Pro	Val	Leu	Tyr	Asp	Thr	Lys	Ala	Thr	Thr	Ser	Lys	Leu	Ile	115	120	125	
Lys	Phe	Glu	Ala	Phe	Leu	Gln	Asn	Ile	130	135									

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1462 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTT	60
TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA	120
TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAA GCTAAAGCCA TTGATGAAGC	180
tGGAATTGAT GCTGACAATG TCCTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC	240
TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT	300
TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA	360
CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA	420
CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCGCGG CAGCTGTAGC	480

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CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCCATCC GCCAACCTGC 540  
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT 600  
 CATTGCCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660  
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720  
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780  
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840  
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900  
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960  
 CTTCGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020  
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080  
 TTTCAGTCTT TCATCAGGTT ACTATGATGC CTACTACAAA AAGGCTGGTC AAGTCCGTAC 1140  
 CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200  
 TGCTCCAAGT GTTGCCATATG ACTTGGAATC TCTCAACCAT GACCCAGTTG CCATGTACTT 1260  
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCCTGC 1320  
 TGGATTCTCT CAAGGTCTAC CTGTCGGAAT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380  
 AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440  
 CGTGATTTTT GGAGGTGACA AC 1462

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 487 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Phe Asn Asn Lys Thr Ile Glu Glu Leu His Asn Leu Leu Val Ser  
 1 5 10 15  
 Lys Glu Ile Ser Ala Thr Glu Leu Thr Gln Ala Thr Leu Glu Asn Ile  
 20 25 30  
 Lys Ser Arg Glu Glu Ala Leu Asn Ser Phe Val Thr Ile Ala Glu Glu  
 35 40 45  
 Gln Ala Leu Val Gln Ala Lys Ala Ile Asp Glu Ala Gly Ile Asp Ala  
 50 55 60  
 Asp Asn Val Leu Ser Gly Ile Pro Leu Ala Val Lys Asp Asn Ile Ser  
 65 70 75 80

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Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr  
 85 90 95  
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly  
 100 105 110  
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly  
 115 120 125  
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His  
 130 135 140  
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala  
 145 150 155 160  
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile  
 165 170 175  
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr  
 180 185 190  
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp  
 195 200 205  
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Asn Ala Leu Leu Leu  
 210 215 220  
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val  
 225 230 235 240  
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met  
 245 250 255  
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu  
 260 265 270  
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly  
 275 280 285  
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala  
 290 295 300  
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg  
 305 310 315 320  
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu  
 325 330 335  
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val  
 340 345 350  
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr  
 355 360 365  
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln  
 370 375 380  
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr  
 385 390 395 400  
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val  
 405 410 415

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Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly  
 420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val  
 435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln  
 450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro  
 465 470 475 480

Val Ile Phe Gly Gly Asp Asn  
 485

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAACACTAC AAGTCGGCGA CAAGGCGCTT GATTTTTCTC TTACTACAAC 60

AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT 120

TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC 180

TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG 240

TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC 300

TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT 360

TGTCCTCGAT ACTGACAATA CGATTCGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA 420

GCCAAACTTC GAA 433

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser  
 1 5 10 15

Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly  
 20 25 30

Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys

35	40	45
Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn		
50	55	60
Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg		
65	70	75 80
Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr		
	85	90 95
Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp		
	100	105 110
His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile		
	115	120 125
Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu		
	130	135 140

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA	60
ACAAGACGTT CCCAATTTTG GTTACAANGA TCCAAGACC GGTACTTATT CTGGTATCGA	120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT	180
TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC	240
CTTTACCATC ACGGACGAAC GCAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA	300
CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAAATCAAA AAGATTGAGG ACCTAAACGG	360
CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA	420
AAAGAAAGGT CTGAAGTTTA AATTCGTCGA ACTTGGTTCC TACCCAGAAT TGATTACTTC	480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC	540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC	600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA	660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC	720
AGAT	724

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val  
1 5 10 15  
Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys  
20 25 30  
Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala  
35 40 45  
Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr  
50 55 60  
Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr  
65 70 75 80  
Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro  
85 90 95  
Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile  
100 105 110  
Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly  
115 120 125  
Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu  
130 135 140  
Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser  
145 150 155 160  
Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu  
165 170 175  
Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys  
180 185 190  
Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn  
195 200 205  
Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu  
210 215 220  
Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala  
225 230 235 240  
Asp

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTC TTgACTTTCA CTATCTCTCA 60  
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120  
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAAT TTGGTGAAGA 180  
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240  
 AGAAGCTGGT CTTGAAGTGG TTGCCCCAACC AAAAATTGAC GTAACCTCAA TGGAAAAAGG 300  
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360  
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCTGAAGA 420  
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480  
 AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCTATC GACGGTGTTG AATTTGACGG 540  
 TGGAAAAGGT GAAAACTTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600  
 AGACCAATTG GTAGGTCACT CAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCCCAGA 660  
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720  
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAGACA TTGATGAAGA 780  
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840  
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900  
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960  
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020  
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080  
 CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140  
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGACACAAG TTCAAACTT 1200  
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260  
 AAGCACAGCA ACAGTAAAA 1279

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

1	5	10	15
Thr Ile Ser Gln Asp Gln Ile Lys Pro Glu Leu Asp Arg Val Phe Lys	20	25	30
Ser Val Lys Lys Ser Leu Asn Val Pro Gly Phe Arg Lys Gly His Leu	35	40	45
Pro Arg Pro Ile Phe Asp Gln Lys Phe Gly Glu Glu Ala Leu Tyr Gln	50	55	60
Asp Ala Met Asn Ala Leu Leu Pro Asn Ala Tyr Glu Ala Ala Val Lys	65	70	75
Glu Ala Gly Leu Glu Val Val Ala Gln Pro Lys Ile Asp Val Thr Ser	85	90	95
Met Glu Lys Gly Gln Asp Trp Val Ile Thr Ala Glu Val Val Thr Lys	100	105	110
Pro Glu Val Lys Leu Gly Asp Tyr Lys Asn Leu Glu Val Ser Val Asp	115	120	125
Val Glu Lys Glu Val Thr Asp Ala Asp Val Glu Glu Arg Ile Glu Arg	130	135	140
Glu Arg Asn Asn Leu Ala Glu Leu Val Ile Lys Glu Ala Ala Ala Glu	145	150	155
Asn Gly Asp Thr Val Val Ile Asp Phe Val Gly Ser Ile Asp Gly Val	165	170	175
Glu Phe Asp Gly Gly Lys Gly Glu Asn Phe Ser Leu Gly Leu Gly Ser	180	185	190
Gly Gln Phe Ile Pro Gly Phe Glu Asp Gln Leu Val Gly His Ser Ala	195	200	205
Gly Glu Thr Val Asp Val Ile Val Thr Phe Pro Glu Asp Tyr Gln Ala	210	215	220
Glu Asp Leu Ala Gly Lys Glu Ala Lys Phe Val Thr Thr Ile His Glu	225	230	235
Val Lys Ala Lys Glu Val Pro Ala Leu Asp Asp Glu Leu Ala Lys Asp	245	250	255
Ile Asp Glu Glu Val Glu Thr Leu Ala Asp Leu Lys Glu Lys Tyr Ser	260	265	270
Lys Glu Leu Ala Ala Ala Lys Glu Glu Ala Tyr Lys Asp Ala Val Glu	275	280	285
Gly Ala Ala Ile Asp Thr Ala Val Glu Asn Ala Glu Ile Val Glu Leu	290	295	300
Pro Glu Glu Met Ile His Glu Glu Val His Arg Ser Val Asn Glu Phe	305	310	315
Leu Gly Asn Leu Gln Arg Gln Gly Ile Asn Pro Asp Met Tyr Phe Gln	325	330	335
Ile Thr Gly Thr Thr Gln Glu Asp Leu His Asn Gln Tyr Gln Ala Glu			

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350

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys  
420 425

TGGTCAAAAAG	GAAAGTCAGA	CAGGAAAGGG	GATGAAAATT	GTGACCAGTT	TTTATCCTAT	60
CTACGCTATG	GTTAAGGAAG	TATCTGGTGA	CTTGAATGAT	GTTCGGATGA	TTCAGTCAAG	120
TAGTGGTATT	CACTCCTTTG	AACCTTCGGC	AAATGATATC	GCAGCCATCT	ATGATGCAGA	180
TGTCTTTGTT	TACCATTCTC	ATACACTCGA	ATCTTGGGCA	GGAAGTCTGG	ATCCAAATCT	240
AAAAAAATCC	AAAGTGAAGG	TCTTAGAGGC	TTCTGAGGGA	ATGACCTTGG	AACGTGTCCC	300
TGGACTAGAG	GATGTGGAAG	CAGGGGATGG	AGTTGATGAA	AAAACGCTCT	ATGACCCCTCA	360
CACATGGCTA	GATCCTGAAA	AAGCTGGAGA	AGAAGCCCCA	ATTATCGCTG	ATAAACTTTC	420
AGAGGTGGAT	AGTGAGCATA	AAGAGACTTA	TCAAAAAAAT	GCGCAACCTT	TATCAAAAAA	480
GCTCAGGAAT						490

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser  
1 5 10 15

[illegible]

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn  
                     20                    25                    30  
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro  
                     35                    40                    45  
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr  
                     50                    55                    60  
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu  
                     65                    70                    75                    80  
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu  
                     85                    90                    95  
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp  
                     100                    105                    110  
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala  
                     115                    120                    125  
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser  
                     130                    135                    140  
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys  
                     145                    150                    155                    160  
 Leu Arg Asn

## (2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1006 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT 60  
 GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG 120  
 TTTTGGTGGC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG 180  
 TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT 240  
 TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT 300  
 TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC 360  
 AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA 420  
 CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA 480  
 TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC 540  
 AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCCGTGC 600  
 CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA 660

TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720  
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780  
 TCCTGTAAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840  
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900  
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960  
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser  
 1 5 10 15  
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala  
 20 25 30  
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val  
 35 40 45  
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala  
 50 55 60  
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val  
 65 70 75 80  
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala  
 85 90 95  
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn  
 100 105 110  
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu  
 115 120 125  
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val  
 130 135 140  
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp  
 145 150 155 160  
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu  
 165 170 175  
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln  
 180 185 190  
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

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195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn		
210	215	220
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser		
225	230	235 240
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala		
	245	250 255
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala		
	260	265 270
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val		
	275	280 285
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met		
	290	295 300
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly		
305	310	315 320
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu		
	325	330 335

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTTCTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACTTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTAACCTAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCTC CAACTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780

TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840  
 TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAAACTAAAG TTCTTGACGT 900  
 TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACTGTC 960  
 ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC 1000

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala  
 1 5 10 15  
 Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn  
 20 25 30  
 Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr  
 35 40 45  
 Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe  
 50 55 60  
 Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu  
 65 70 75 80  
 Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr  
 85 90 95  
 Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly  
 100 105 110  
 Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr  
 115 120 125  
 Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val  
 130 135 140  
 Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys  
 145 150 155 160  
 Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile  
 165 170 175  
 His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly  
 180 185 190  
 Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn  
 195 200 205  
 Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn  
 210 215 220

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 T022T0 2229260

(2) INFORMATION FOR SEQ ID NO: 55:

(A) LENGTH: 2389 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TTCTTACGAG	TTGGGACTGT	ATCAAGCTAG	AACGGTTAAG	GAAATAATC	GTGTTTCCTA	60
TATAGATGGA	AAACAAGCGA	CGCAAAAAAC	GGAGAATTTG	ACTCCTGATG	AGGTTAGCAA	120
GCGTGAAGGA	ATCAATGCTG	AGCAAATCGT	CATCAAGATA	ACAGACCAAG	GCTATGTCAC	180
TTCACATGGC	GACCACTATC	ATTATTACAA	TGGTAAGGTT	CCTTATGACG	CTATCATCAG	240
TGAAGAATTA	CTCATGAAAG	ATCCAAACTA	TAAGCTAAAA	GATGAGGATA	TTGTTAATGA	300
GGTCAAGGGT	GGATATGTTA	TCAAGGTAGA	TGGAAAATAC	TATGTTTACC	TTAAGGATGC	360
TGCCCACGCG	GATAACGTCC	GTACAAAAGA	GGAAATCAAT	CGACAAAAAC	AAGAGCATAG	420
TCAACATCGT	GAAGGTGGAA	CTCCAAGAAA	CGATGGTGCT	GTTGCCTTGG	CACGTTTCGA	480
AGGACGCTAT	ACTACAGATG	ATGGTTATAT	CTTTAATGCT	TCTGATATCA	TAGAGGATAC	540
TGGTGATGCT	TATATCGTTC	CTCATGGAGA	TCATTACCAT	TACATTCCCTA	AGAATGAGTT	600
ATCAGCTAGC	GAGTTGGCTG	CTGCAGAAGC	CTTCCTATCT	GGTCGAGGAA	ATCTGTCAAA	660
TTCAAGAACC	TATCGCCGAC	AAAATAGCGA	TAACACTTCA	AGAACAACT	GGGTACCTTC	720
TGTAAGCAAT	CCAGGAACTA	CAAATACTAA	CACAAGCAAC	AACAGCAACA	CTAACAGTCA	780
AGCAAGTCAA	AGTAATGACA	TTGATAGTCT	CTTGAAACAG	CTCTACAAAC	TGCCTTTGAG	840
TCAACGACAT	GTAGAATCTG	ATGGCCTTGT	CTTTGATCCA	GCACAAATCA	CAAGTCGAAC	900
AGCTAGAGGT	GTTGCAGTGC	CACACGGAGA	TCATTACCAC	TTCATCCCTT	ACTCTCAAAAT	960

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020  
 GGTACCAGAT TCAAGGCCAG AACACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080  
 CCCGCAACCT GCACCAAATC TTAAAATAGA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT 1140  
 ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200  
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAGAGAG 1260  
 TGTTCACAC ACTTTAACTG CTAAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320  
 TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNA AATAAGGGTCG 1380  
 TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440  
 TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG 1500  
 ACTTGGCAAA CCAAATTCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560  
 AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTGTGAT GAACATGATA TAATCAGTGA 1620  
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680  
 CCTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740  
 TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAGTGA GATAGTGCAG CAGCTATTTA 1800  
 CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860  
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT 1920  
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGAAGA 1980  
 TTTGTTTGGC ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040  
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100  
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160  
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220  
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAACT CTAGCTGGTT TACGAAATAA 2280  
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340  
 GTTGTTAAAA GGAAGTAATC CTTATCTGT AAGTAAGGAA AAAATAAAC 2389

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

1	5	10	15
Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu Asn	20	25	30
Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu Gln	35	40	45
Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp	50	55	60
His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile Ser	65	70	75
Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Lys Leu Lys Asp Glu Asp	85	90	95
Ile Val Asn Glu Val Lys Gly Gly Tyr Val Ile Lys Val Asp Gly Lys	100	105	110
Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr	115	120	125
Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg Glu	130	135	140
Gly Gly Thr Pro Arg Asn Asp Gly Ala Val Ala Leu Ala Arg Ser Gln	145	150	155
Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile	165	170	175
Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr	180	185	190
His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala	195	200	205
Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu Ser Asn Ser Arg Thr Tyr	210	215	220
Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg Thr Asn Trp Val Pro Ser	225	230	235
Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser Asn	245	250	255
Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu Lys	260	265	270
Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp Gly	275	280	285
Leu Val Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly Val	290	295	300
Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met	305	310	315
Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg	325	330	335
Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln			

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675	680	685
Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys		
690	695	700
Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro		
705	710	715 720
Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val		
725	730	735
Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu		
740	745	750
Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn		
755	760	765
Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly		
770	775	780
Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn		
785	790	795

## (2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA	60
TAGTTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TGCGTTTTGT	120
TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATTCTG CGGTATTAGC	180
TGAGAAATAC AATCGTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT	240
TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA	300
TGTTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA	360
TTTTAATGGA GACCAGTTGA CTAGTTTTCT GAAACATCAA TCTGGGGATC AGGCTAGTCA	420
ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA	480
GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC	540
TCGTTTTAAT GAACGCCAAG CTTCCTTTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA	600
CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC	660
AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT	720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTTG AAGAAATTAA AGGATTCTCA	780
GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA	840

(2) INFORMATION FOR SEQ ID NO:58:

(A) LENGTH: 393 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr	Glu	Met	His	His	Asn	Leu	Gly	Ala	Glu	Lys	Arg	Ser	Ala	Val	Ala
1			5						10					15	
Thr	Thr	Ile	Asp	Ser	Phe	Lys	Glu	Arg	Ser	Gln	Lys	Val	Arg	Ala	Leu
		20						25					30		
Ser	Asp	Pro	Asn	Val	Arg	Phe	Val	Pro	Phe	Phe	Gly	Ser	Ser	Glu	Trp
		35					40					45			
Leu	Arg	Phe	Asp	Gly	Ala	His	Ser	Ala	Val	Leu	Ala	Glu	Lys	Tyr	Asn
	50					55					60				
Arg	Ser	Tyr	Arg	Pro	Tyr	Leu	Leu	Gly	Gln	Gly	Gly	Ala	Ala	Ser	Leu
65					70					75					80
Asn	Gln	Tyr	Phe	Gly	Met	Gln	Gln	Met	Leu	Pro	Gln	Leu	Glu	Asn	Lys
				85					90					95	
Gln	Val	Val	Tyr	Val	Ile	Ser	Pro	Gln	Trp	Phe	Ser	Lys	Asn	Gly	Tyr
			100					105					110		
Asp	Pro	Ala	Ala	Phe	Gln	Gln	Tyr	Phe	Asn	Gly	Asp	Gln	Leu	Thr	Ser
		115					120					125			
Phe	Leu	Lys	His	Gln	Ser	Gly	Asp	Gln	Ala	Ser	Gln	Tyr	Ala	Ala	Thr
	130					135					140				
Arg	Leu	Leu	Gln	Gln	Phe	Pro	Asn	Val	Ala	Met	Lys	Asp	Leu	Val	Gln
145					150					155					160
Lys	Leu	Ala	Ser	Lys	Glu	Glu	Leu	Ser	Thr	Ala	Asp	Asn	Glu	Met	Ile
				165					170					175	
Glu	Leu	Leu	Ala	Arg	Phe	Asn	Glu	Arg	Gln	Ala	Ser	Phe	Phe	Gly	Gln
			180					185					190		
Phe	Ser	Val	Arg	Gly	Tyr	Val	Asn	Tyr	Asp	Lys	His	Val	Ala	Lys	Tyr
		195					200					205			

Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val  
 210 215 220  
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met  
 225 230 235 240  
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu  
 245 250 255  
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn  
 260 265 270  
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro  
 275 280 285  
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly  
 290 295 300  
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln  
 305 310 315 320  
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly  
 325 330 335  
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly  
 340 345 350  
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr  
 355 360 365  
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp  
 370 375 380  
 Ala Thr Tyr Asp Gly Asp Val Lys Glu  
 385 390

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTACTATCAA	300
GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420

AAAACTTTCC GCTTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGA CTGAGAC 480  
 TTCCTTCAGT CCACTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540  
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600  
 TGAAGTGATT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660  
 GGAAAAAGAG TTA CTGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720  
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780  
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840  
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT 900  
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960  
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020  
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080  
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAT GAGGAATTGA CCTTTAAAT 1140  
 GGCCCCAAG GAGGAAC TTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200  
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260  
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320  
 CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCAC TTAC ACAGGACAAA AGACCCCTCCG 1380  
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln  
 1 5 10 15  
 Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu  
 20 25 30  
 Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys  
 35 40 45  
 His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu  
 50 55 60  
 Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu  
 65 70 75 80  
 Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

85

90

95

Phe Thr Ile Lys Asp Glu Lys Leu Phe Glu Ile Leu Gln Thr Gln Glu  
 100 105 110  
 Leu Thr Ala Lys Asn Leu Gln Ser Leu Phe Gln Gly Leu Gly Arg Asp  
 115 120 125  
 Thr Ala Asn Glu Leu Glu Arg Ile Leu Val Ser Glu Lys Leu Ser Ala  
 130 135 140  
 Phe Arg Asn Phe Phe Asn Gln Glu Thr Lys Pro Cys Leu Thr Glu Thr  
 145 150 155 160  
 Ser Phe Ser Pro Val Pro Phe Ala Asn Gln Val Gly Glu Pro Phe Ala  
 165 170 175  
 Asn Leu Ser Asp Leu Leu Asp Thr Tyr Tyr Lys Asp Lys Ala Glu Arg  
 180 185 190  
 Asp Arg Val Lys Gln Gln Ala Ser Glu Leu Ile Arg Arg Val Glu Asn  
 195 200 205  
 Glu Leu Gln Lys Asn Arg His Lys Leu Lys Lys Gln Glu Lys Glu Leu  
 210 215 220  
 Leu Ala Thr Asp Asn Ala Glu Glu Phe Arg Gln Lys Gly Glu Leu Leu  
 225 230 235 240  
 Thr Thr Phe Leu His Gln Val Pro Asn Asp Gln Asp Gln Val Ile Leu  
 245 250 255  
 Asp Asn Tyr Tyr Thr Asn Gln Pro Ile Met Ile Ala Leu Asp Lys Ala  
 260 265 270  
 Leu Thr Pro Asn Gln Asn Ala Gln Arg Tyr Phe Lys Arg Tyr Gln Lys  
 275 280 285  
 Leu Lys Glu Ala Val Lys Tyr Leu Thr Asp Leu Ile Glu Glu Thr Lys  
 290 295 300  
 Ala Thr Ile Leu Tyr Leu Glu Ser Val Glu Thr Val Leu Asn Gln Ala  
 305 310 315 320  
 Gly Leu Glu Glu Ile Ala Glu Ile Arg Glu Glu Leu Ile Gln Thr Gly  
 325 330 335  
 Phe Ile Arg Arg Arg Gln Arg Glu Lys Ile Gln Lys Arg Lys Lys Leu  
 340 345 350  
 Glu Gln Tyr Leu Ala Ser Asp Gly Lys Thr Ile Ile Tyr Val Gly Arg  
 355 360 365  
 Asn Asn Leu Gln Asn Glu Glu Leu Thr Phe Lys Met Ala Arg Lys Glu  
 370 375 380  
 Glu Leu Trp Phe His Ala Lys Asp Ile Pro Gly Ser His Val Val Ile  
 385 390 395 400  
 Ser Gly Asn Leu Asp Pro Ser Asp Ala Val Lys Thr Asp Ala Ala Glu  
 405 410 415  
 Leu Ala Ala Tyr Phe Ser Gln Gly Arg Leu Ser Asn Leu Val Gln Val

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173

420

425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro  
435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp  
450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser  
465 470

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA	60
AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC	120
CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC	180
ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG	240
TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA	300
AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT	360
TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT	420
AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT	480
CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA	540
TGCC	544

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys	
1 5 10 15	

Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn	20 25 30
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Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln	
---	--

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35	40	45
Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg		
50	55	60
Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys		
65	70	75 80
Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp		
	85	90 95
Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro		
	100	105 110
Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys		
	115	120 125
Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr		
	130	135 140
Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile		
	145	150 155 160
Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu		
	165	170 175
Leu Gln Pro Tyr Ala		
	180	

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA	60
GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA	120
CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA	180
GTATGTCAGC CGTGGTGGTT TGAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT	240
GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT	300
ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGA	360
ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCGCT ATGCTGAAAA	420
GACTGATTTT GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG	480
TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT	540
CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC	600
TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC	660

(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 270 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala	Lys	Glu	Arg	Val	Asp	Val	Leu	Ala	Tyr	Lys	Gln	Gly	Leu	Phe	Glu
1				5					10					15	
Thr	Arg	Glu	Gln	Ala	Lys	Arg	Gly	Val	Met	Ala	Gly	Leu	Val	Val	Ala
			20					25					30		
Val	Leu	Asn	Gly	Glu	Arg	Phe	Asp	Lys	Pro	Gly	Glu	Lys	Ile	Pro	Asp
		35					40					45			
Asp	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Glu	Lys	Leu	Lys	Tyr	Val	Ser	Arg
	50					55					60				
Gly	Gly	Leu	Lys	Leu	Glu	Lys	Ala	Leu	Gln	Val	Phe	Asp	Leu	Ser	Val
65					70				75						80
Asp	Gly	Ala	Thr	Thr	Ile	Asp	Ile	Gly	Ala	Ser	Thr	Gly	Gly	Phe	Thr
				85					90					95	
Asp	Val	Met	Leu	Gln	Asn	Ser	Ala	Lys	Leu	Val	Phe	Ala	Val	Asp	Val
			100					105					110		
Gly	Thr	Asn	Gln	Leu	Ala	Trp	Lys	Leu	Arg	Gln	Asp	Pro	Arg	Val	Val
		115					120					125			
Ser	Met	Glu	Gln	Phe	Asn	Phe	Arg	Tyr	Ala	Glu	Lys	Thr	Asp	Phe	Glu
	130					135					140				
Gln	Glu	Pro	Ser	Phe	Ala	Ser	Ile	Asp	Val	Ser	Phe	Ile	Ser	Leu	Ser
145					150					155					160
Leu	Ile	Leu	Pro	Ala	Leu	His	Arg	Val	Leu	Ala	Asp	Gln	Gly	Gln	Val
				165					170					175	
Val	Ala	Leu	Val	Lys	Pro	Gln	Phe	Glu	Ala	Gly	Arg	Glu	Gln	Ile	Gly
			180					185					190		
Lys	Asn	Gly	Ile	Ile	Arg	Asp	Ala	Lys	Val	His	Gln	Asn	Val	Leu	Glu
		195					200					205			
Ser	Val	Thr	Ala	Met	Ala	Val	Glu	Val	Gly	Phe	Ser	Val	Leu	Gly	Leu
		210				215					220				
Asp	Phe	Ser	Pro	Ile	Gln	Gly	Gly	His	Gly	Asn	Ile	Glu	Phe	Leu	Ala
225					230					235					240

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile  
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu  
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCTAT GAACCTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT	60
TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT	120
CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA	180
TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTTCCCTT ATGATGCCAT	240
CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT	300
CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAAACGGT AAATACTATG TNTACCTTAA	360
GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA	420
ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG	480
ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG	540
TGATGCTTAT ATCGTTCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC	600
AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCTTTC	660
TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT	720
GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA	780
ATTGTATGCT AAACCCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC	840
AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA	900
CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATTCCCCT	960
TCGTTATCGT TCAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC	1020
GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAAT CCTCAACCAG CTCCAAGCAA	1080
TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTTCGAAAA GTAGGCGATG GTTATGTCTT	1140
TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AAACAGCAGC	1200
AGGCATTGAT AGCAAATGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA	1260
AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG	1320

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AATTCACCAA GATTTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380  
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440  
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500  
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560  
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620  
 TATGACCCAT AGCCACTGGA TTAAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680  
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTCAGG 1740  
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800  
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860  
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920  
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980  
 CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040  
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100  
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160  
 ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220  
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGAAAA 2280  
 AATCCAGGAT 2290

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 763 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu  
 1 5 10 15  
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala  
 20 25 30  
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala  
 35 40 45  
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His  
 50 55 60  
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile  
 65 70 75 80  
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

85

90

95

Ser	Asp	Ile	Val	Asn	Glu	Ile	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asn
			100					105					110		
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile
		115					120					125			
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	Arg	Ser	His	Asn
	130					135					140				
His	Asn	Ser	Arg	Ala	Asp	Asn	Ala	Val	Ala	Ala	Ala	Arg	Ala	Gln	Gly
145					150				155						160
Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile	Ile
				165					170					175	
Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	His
		180						185					190		
Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Glu
		195					200					205			
Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser	Ser
	210					215					220				
Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn	Leu
225					230					235					240
Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser
				245					250					255	
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu
			260					265					270		
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala
		275					280					285			
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr
	290					295					300				
Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu
305					310					315					320
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro
				325					330					335	
Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro
			340					345					350		
Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys
		355					360					365			
Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly
	370					375					380				
Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala
385					390					395					400
Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu
				405					410					415	
Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn

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420	425	430
Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn 435 440 445		
Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg 450 455 460		
Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu 465 470 475 480		
Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn 485 490 495		
Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala 500 505 510		
Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile 515 520 525		
Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser 530 535 540		
His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala 545 550 555 560		
Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His 565 570 575		
Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn 580 585 590		
Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn 595 600 605		
Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His 610 615 620		
Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu 625 630 635 640		
Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val 645 650 655		
Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly 660 665 670		
Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala 675 680 685		
Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu 690 695 700		
Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys 705 710 715 720		
Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu 725 730 735		
Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg 740 745 750		
Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp		

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755

760

## (2) INFORMATION FOR SEQ ID NO: 67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA      60
AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAAACCTGT      120
ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA      180
AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA      240
TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT      300
TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG              352

```

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile
1           5           10           15
Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser
          20           25           30
Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys
          35           40           45
Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn
          50           55           60
Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp
          65           70           75           80
Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val
          85           90           95
Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr
          100          105          110
Asn Asn Pro Asn Lys
          115

```

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## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG	60
TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA	120
AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC	180
GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA	240
AAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA	300
ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT	360
TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC	420
TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT	480
TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT	540
AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA	600
GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC	660
TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA	720
TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT	780
ACCTTGAAAA AATGGTGTTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA	840
GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG	900
TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA	960
GAGTGCATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCGG	1020
TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA	1080
TCAATGAAAA AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTTCTGCTAA	1140
AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT	1200
TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC	1260
AGGATGGCTT CAATATATGG GGCAATGGTA TACTTTGCT CCATCAGGGG AA	1312

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn
1           5           10           15
Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu Glu Ser Asn Gly His
20           25           30
Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp Phe Pro Asp Gly Ser
35           40           45
Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu Thr Ser Tyr Lys His
50           55           60
Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys Glu Leu Gly Val Gln
65           70           75           80
Lys Leu Asp Phe Ile Leu Val Thr His Thr His Ser Asp His Ile Gly
85           90           95
Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val Asp Arg Val Tyr Leu
100          105          110
Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser Glu Arg Leu Trp Asp
115          120          125
Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr Ala Ala Glu Lys Gly
130          135          140
Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp Ala His Phe Gln Phe
145          150          155          160
Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu Asn Glu Thr Asp Ser
165          170          175
Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn Ser Asn Ser Leu Ile
180          185          190
Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr Leu Gly Gly Asp Leu
195          200          205
Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly Pro Leu Ile Gly Lys
210          215          220
Val Asp Leu Met Lys Phe Asn His His His Asp Thr Asn Lys Ser Asn
225          230          235          240
Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser Leu Ile Val Gln Thr
245          250          255
Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp Ser Glu Tyr Val Asn
260          265          270
Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn Ala Ala Ser Lys Asp
275          280          285
Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp Gly Phe Val Asn Ile
290          295          300

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Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys  
 305 310 315 320

Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu  
 325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn  
 340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His  
 355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys  
 370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile  
 385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly  
 405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe  
 420 425 430

Ala Pro Ser Gly Glu  
 435

## (2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1855 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGCGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780  
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCCTCTTT GACATCATTG CCCAGTCTAT 840  
 CAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900  
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG 960  
 ACGTACTAAA CAATTCCGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020  
 AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080  
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140  
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200  
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260  
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320  
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCCGATG AAAAAGCTCG 1380  
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440  
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500  
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAATG GAACTAGCCA 1560  
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA 1620  
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680  
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740  
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTT GAAACGAATC 1800  
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe  
 1 5 10 15  
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser  
 20 25 30  
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu  
 35 40 45  
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala  
 50 55 60

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Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala  
 65 70 75 80  
 Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu  
 85 90 95  
 Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro  
 100 105 110  
 Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr  
 115 120 125  
 Lys Arg Leu Leu Ile Asp Ser Ile Lys Tyr Leu Val Asp Thr Tyr Lys  
 130 135 140  
 Val Asp Gly Phe Arg Phe Asp Met Met Gly Asp His Asp Ala Ala Ser  
 145 150 155 160  
 Ile Glu Glu Ala Tyr Lys Ala Ala Arg Ala Leu Asn Pro Asn Leu Ile  
 165 170 175  
 Met Leu Gly Glu Gly Trp Arg Thr Tyr Ala Gly Asp Glu Asn Met Pro  
 180 185 190  
 Thr Lys Ala Ala Asp Gln Asp Trp Met Lys His Thr Asp Thr Val Ala  
 195 200 205  
 Val Phe Ser Asp Asp Ile Arg Asn Asn Leu Lys Ser Gly Tyr Pro Asn  
 210 215 220  
 Glu Gly Gln Pro Ala Phe Ile Thr Gly Gly Lys Arg Asp Val Asn Thr  
 225 230 235 240  
 Ile Phe Lys Asn Leu Ile Ala Gln Pro Thr Asn Phe Glu Ala Asp Ser  
 245 250 255  
 Pro Gly Asp Val Ile Gln Tyr Ile Ala Ala His Asp Asn Leu Thr Leu  
 260 265 270  
 Phe Asp Ile Ile Ala Gln Ser Ile Lys Lys Asp Pro Ser Lys Ala Glu  
 275 280 285  
 Asn Tyr Ala Glu Ile His Arg Arg Leu Arg Leu Gly Asn Leu Met Val  
 290 295 300  
 Leu Thr Ala Gln Gly Thr Pro Phe Ile His Ser Gly Gln Glu Tyr Gly  
 305 310 315 320  
 Arg Thr Lys Gln Phe Arg Asp Pro Ala Tyr Lys Thr Pro Val Ala Glu  
 325 330 335  
 Asp Lys Val Pro Asn Lys Ser His Leu Leu Arg Asp Lys Asp Gly Asn  
 340 345 350  
 Pro Phe Asp Tyr Pro Tyr Phe Ile His Asp Ser Tyr Asp Ser Ser Asp  
 355 360 365  
 Ala Val Asn Lys Phe Asp Trp Thr Lys Ala Thr Asp Gly Lys Ala Tyr  
 370 375 380  
 Pro Glu Asn Val Lys Ser Arg Asp Tyr Met Lys Gly Leu Ile Ala Leu  
 385 390 395 400

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Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys  
 405 410 415  
 Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys  
 420 425 430  
 Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile  
 435 440 445  
 Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu  
 450 455 460  
 Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu  
 465 470 475 480  
 Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp  
 485 490 495  
 Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg  
 500 505 510  
 Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro  
 515 520 525  
 Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro  
 530 535 540  
 Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro  
 545 550 555 560  
 Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala  
 565 570 575  
 Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val  
 580 585 590  
 Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn  
 595 600 605  
 Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu  
 610 615

## (2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300

AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360  
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420  
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480  
 AGTACAGCAA GGTGGCTTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540  
 TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600  
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660  
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA 720  
 CTA CTTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780  
 GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840  
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900  
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960  
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020  
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080  
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140  
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200  
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260  
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320  
 TTTCAAAGAT TTAACAGAGG CTACAAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380  
 TTTGCTAAAC ATTAACAATA GCCTTTTGGG GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440  
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG 1500  
 GGGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560  
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620  
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGGAAGAACT TTCCTTGGA ACAAGGCTTC 1680  
 TGGTATGAAT GTGGAATATG CTTGAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740  
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

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Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser  
 1 5 10 15  
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe  
 20 25 30  
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln  
 35 40 45  
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser  
 50 55 60  
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly  
 65 70 75 80  
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr  
 85 90 95  
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala  
 100 105 110  
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu  
 115 120 125  
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu  
 130 135 140  
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys  
 145 150 155 160  
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr  
 165 170 175  
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn  
 180 185 190  
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu  
 195 200 205  
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys  
 210 215 220  
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr  
 225 230 235 240  
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp  
 245 250 255  
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys  
 260 265 270  
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser  
 275 280 285  
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly  
 290 295 300  
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala  
 305 310 315 320  
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly  
 325 330 335

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Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys  
 340 345 350  
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu  
 355 360 365  
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys  
 370 375 380  
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr  
 385 390 395 400  
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met  
 405 410 415  
 Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly  
 420 425 430  
 Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr  
 435 440 445  
 Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile  
 450 455 460  
 Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu  
 465 470 475 480  
 Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu  
 485 490 495  
 Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe  
 500 505 510  
 Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr  
 515 520 525  
 Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys  
 530 535 540  
 Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser  
 545 550 555 560  
 Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile  
 565 570 575  
 Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp  
 580 585 590

## (2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:-----

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA

CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA 120  
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC 180  
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC 240  
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT 300  
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTTG CTACTAAATA 360  
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG 420  
GAAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG 480  
TACTTTAAGT CAAAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAAGaA CCArkCCCCA 540  
AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA 600  
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660  
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT 720  
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780  
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840  
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900  
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960  
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020  
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080  
CAATGATAAT GGTGAATGGG TCGCT 1105

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile  
1 5 10 15  
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr  
20 25 30  
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr  
35 40 45  
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp  
50 55 60  
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro  
65 70 75 80

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Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala  
 85 90 95  
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val  
 100 105 110  
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala  
 115 120 125  
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr  
 130 135 140  
 Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser  
 145 150 155 160  
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg  
 165 170 175  
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr  
 180 185 190  
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly  
 195 200 205  
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg  
 210 215 220  
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met  
 225 230 235 240  
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val  
 245 250 255  
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser  
 260 265 270  
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro  
 275 280 285  
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr  
 290 295 300  
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr  
 305 310 315 320  
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val  
 325 330 335  
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn  
 340 345 350  
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 661 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTTATC TCCAACATTA 60  
TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120  
ACCTAATGCT CAGGCTGTTT ACTTGTTGGG TGATTTTACC AACTGGATTG AAAATCAGAT 180  
TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240  
GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300  
TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360  
GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420  
TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480  
TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTAT CTCGTTGAAA TGAATATAC 540  
TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600  
TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660  
C 661

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr  
1 5 10 15  
Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His  
20 25 30  
Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu  
35 40 45  
Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg  
50 55 60  
Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly  
65 70 75 80  
His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met  
85 90 95  
Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly  
100 105 110  
Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155 160
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
165	170	175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
180	185	190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
195	200	205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
210	215	220

## (2) INFORMATION FOR SEQ ID NO: 79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN	60
TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGGA	180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAGCAT TGGATTGATG TCTATCATTT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTCT CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCAATGAAT GCTAAGATGA AGTATTTCCG	840
TTCTCAGCTA AACCAGTTTT ACAAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA	900
TGATGGTATT GAAATCATTT ATGCGGATAA TCGAGACCAG AGTGTCTTT CCTTTATTCG	960

TAAGGGTAAA AAGGGA

976

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
1           5           10           15

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
          20           25           30

Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
          35           40           45

His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
          50           55           60

Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
65           70           75           80

Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
          85           90           95

Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
          100          105          110

Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
          115          120          125

Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
          130          135          140

Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
          145          150          155          160

Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
          165          170          175

Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
          180          185          190

Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
          195          200          205

His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
          210          215          220

Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
          225          230          235          240

Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
          245          250          255

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Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met  
 260 265 270

Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys  
 275 280 285

Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu  
 290 295 300

Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg  
 305 310 315 320

Lys Gly Lys Lys Gly  
 325

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA 60

AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG 120

GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA 180

AGCCGTAACT CCAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT 240

AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA 300

TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT 360

TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA 420

AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC 480

ACAAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAAC 540

AGATGAAAAA GACCTCAAGA AAAATGTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC 600

TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC 660

ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC 720

AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC 780

TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA 840

ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC 900

GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC 960

TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT 1020

AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC 1080

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CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140  
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA 1200  
 ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260  
 AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAAGTCCAT 1320  
 CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380  
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440  
 ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500  
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC 1560  
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTTAAACG 1620  
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680  
 ATTCCGTTTC GGTAAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740  
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800  
 GATTTATGGA TCAGAAACAT CTTGAGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860  
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920  
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980  
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040  
 GCACAACCAA AATCAAACCTC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100  
 CATTCCAAAA CATGACTTCT ATCTCTACCA AAGC 2134

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys  
 1 5 10 15

Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu  
 20 25 30

Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser  
 35 40 45

Thr Glu Ala Ile-Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro  
 50 55 60

Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

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 102270 225266

65	70	75	80
Glu Ser Gln Ala Ser Asn Gln Glu Lys	Pro Leu Lys Glu Asp Ala Lys		
85	90	95	
Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val			
100	105	110	
Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu			
115	120	125	
Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu			
130	135	140	
Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala			
145	150	155	160
Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys			
165	170	175	
Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr			
180	185	190	
Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu			
195	200	205	
Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr			
210	215	220	
Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala			
225	230	235	240
Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr			
245	250	255	
Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn			
260	265	270	
Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys			
275	280	285	
Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp			
290	295	300	
His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala			
305	310	315	320
Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu			
325	330	335	
Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp			
340	345	350	
Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val			
355	360	365	
Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr			
370	375	380	
Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu			
385	390	395	400
Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu			

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405 410 415  
 Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met  
 420 425 430  
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser  
 435 440 445  
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu  
 450 455 460  
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly  
 465 470 475 480  
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu  
 485 490 495  
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn  
 500 505 510  
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala  
 515 520 525  
 Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val  
 530 535 540  
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys  
 545 550 555 560  
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu  
 565 570 575  
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu  
 580 585 590  
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser  
 595 600 605  
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys  
 610 615 620  
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn  
 625 630 635 640  
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp  
 645 650 655  
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp  
 660 665 670  
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val  
 675 680 685  
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His  
 690 695 700  
 Asp Phe Tyr Leu Tyr Gln Ser  
 705 710

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

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(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAGTGGT AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAAATT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGTCAT AAGCCAGGAG CAGTCACTCT	1680

GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA 1740  
GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800  
AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860  
CACTTGGCAA GCTATTCCGA AAGAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920  
TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980  
AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040  
TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTCCG 2100  
TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA 2160  
ATTAACA 2167

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr	Phe	Gly	Ile	Val	Asp	Thr	Ala	Gly	Ile	Pro	Lys	His	Asp	Phe	Tyr	1	5	10	15
Leu	Tyr	Gln	Ser	Gln	Trp	Val	Ser	Val	Lys	Lys	Lys	Pro	Met	Val	His	20	25	30	
Leu	Leu	Pro	His	Trp	Asn	Trp	Glu	Asn	Lys	Glu	Leu	Ala	Ser	Lys	Val	35	40	45	
Ala	Asp	Ser	Glu	Gly	Lys	Ile	Pro	Val	Arg	Ala	Tyr	Ser	Asn	Ala	Ser	50	55	60	
Ser	Val	Glu	Leu	Phe	Leu	Asn	Gly	Lys	Ser	Leu	Gly	Leu	Lys	Thr	Phe	65	70	75	80
Asn	Lys	Lys	Gln	Thr	Ser	Asp	Gly	Arg	Thr	Tyr	Gln	Glu	Gly	Ala	Asn	85	90	95	
Ala	Asn	Glu	Leu	Tyr	Leu	Glu	Trp	Lys	Val	Ala	Tyr	Gln	Pro	Gly	Thr	100	105	110	
Leu	Glu	Ala	Ile	Ala	Arg	Asp	Glu	Ser	Gly	Lys	Glu	Ile	Ala	Arg	Asp	115	120	125	
Lys	Ile	Thr	Thr	Ala	Gly	Lys	Pro	Ala	Ala	Val	Arg	Leu	Ile	Lys	Glu	130	135	140	
Asp	His	Ala	Ile	Ala	Ala	Asp	Gly	Lys	Asp	Leu	Thr	Tyr	Ile	Tyr	Tyr	145	150	155	160
Glu	Ile	Val	Asp	Ser	Gln	Gly	Asn	Val	Val	Pro	Thr	Ala	Asn	Asn	Leu				

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165

170

175

Val Arg Phe Gln Leu His Gly Gln Gly Gln Leu Val Gly Val Asp Asn  
 180 185 190  
 Gly Glu Gln Ala Ser Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser  
 195 200 205  
 Trp Ile Arg Lys Ala Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser  
 210 215 220  
 Thr Glu Gln Ala Gly Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu  
 225 230 235 240  
 Lys Ser Asn Gln Val Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu  
 245 250 255  
 Lys Thr Val Leu Gly Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly  
 260 265 270  
 Glu Ala Pro Glu Met Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly  
 275 280 285  
 Ser Arg Ala Glu Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys  
 290 295 300  
 Pro Gly Ile Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu  
 305 310 315 320  
 Ala Arg Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys  
 325 330 335  
 Arg Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser  
 340 345 350  
 Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp  
 355 360 365  
 Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg  
 370 375 380  
 Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu  
 385 390 395 400  
 Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr  
 405 410 415  
 Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln  
 420 425 430  
 Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser  
 435 440 445  
 Ala Lys Asn Ala Ala Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly  
 450 455 460  
 Met Arg Ala Ser Ile Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln  
 465 470 475 480  
 Thr Tyr Ala Ile Gln Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu  
 485 490 495  
 Ser Leu Gln Val Glu Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val

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202

500	505	510
Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu 515	520	525
Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala 530	535	540
Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu 545	550	555
Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln 565	570	575
Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val 580	585	590
Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val 595	600	605
Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala 610	615	620
Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly 625	630	635
Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu 645	650	655
Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu 660	665	670
Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His 675	680	685
Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr 690	695	700
Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln 705	710	715
Leu Thr		

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC	120
TCAAAGTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240

CTACAATAAC CAACCAGCCA ATCGTTGGAC AAACCTGGAAT CGTACTAATC CAGAAGCTTC	300
AGTCGGTGTT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG	360
TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA	420
TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTTGGTA ATGAGGACCA	480
TGTCTTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT	540
CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTTCGTAT	600
TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTCG	660
GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT	720
AGCAAACTTC AACCCGTATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC	780
GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA	840
AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG	900
TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTTAAACA	960
AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTC CAGTTTACTT	1020
CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC	1080
GGAAAATCTG AAAAAAGCAG GTCAATTTAC TGTTTCGAGGC CGTGTCCCTG GTAGTAACCT	1140
TGTTGCTGAG ATCACTGTAC GAGTGACAGA CAAACTTGGT GAGACTCTTT CAGATAACCC	1200
TAAGTATGAT GAAAAACAGTA ACCAGGCCTT TGCTTCAGCA ACCAATGATA TTGACAAAAA	1260
CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC	1320
AAACTGGTCA CCAACACCAT CTTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA	1380
AAATGGTAAG ATTGTAGAAC GGACTGTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG	1440
TGGTACGGAT GCACCATCTA AACTCGTTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAGT	1500
GCCAACCTAC TATTCAAACCT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA	1560
AAATTGGGAA GCTGTTCCCTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA	1620
CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA	1680
TAAGAGCGGT GTTGCGATGA TTGAGATGAC CTTCCCTGCA CCAAGTGAAT TGCCTCAAGA	1740
AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTCG CTGAAAATCG	1800
TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA	1860
TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTTCGCC	1920
CGTTTCAGAA AGTGGAAAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAACC	1980
AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CCAAAAATCG AATTTGTTGA	2040
AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAAC	2100

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TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160  
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220  
 GGTGGAACC AAACAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTGAG AAAAAGCAGA 2280  
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu  
 1 5 10 15  
 Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr  
 20 25 30  
 Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile  
 35 40 45  
 Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp  
 50 55 60  
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser  
 65 70 75 80  
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn  
 85 90 95  
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser  
 100 105 110  
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly  
 115 120 125  
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr  
 130 135 140  
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His  
 145 150 155 160  
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala  
 165 170 175  
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys  
 180 185 190  
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys  
 195 200 205  
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala  
 210 215 220

09533 04204  
 T022T0 2259460

Ala	Ala	Lys	Gln	Gly	Gln	Thr	Arg	Ile	Gln	Val	Asp	Gly	Lys	Asp	Leu	225	230	235	240
Ala	Asn	Phe	Asn	Pro	Asp	Leu	Thr	Asp	Tyr	Tyr	Leu	Glu	Ser	Val	Asp	245	250	255	
Gly	Lys	Val	Pro	Ala	Val	Thr	Ala	Ser	Val	Ser	Asn	Asn	Gly	Leu	Ala	260	265	270	
Thr	Val	Val	Pro	Ser	Val	Arg	Glu	Gly	Glu	Pro	Val	Arg	Val	Ile	Ala	275	280	285	
Lys	Ala	Glu	Asn	Gly	Asp	Ile	Leu	Gly	Glu	Tyr	Arg	Leu	His	Phe	Thr	290	295	300	
Lys	Asp	Lys	Ser	Leu	Leu	Ser	His	Lys	Pro	Val	Ala	Ala	Val	Lys	Gln	305	310	315	320
Ala	Arg	Leu	Leu	Gln	Val	Gly	Gln	Ala	Leu	Glu	Leu	Pro	Thr	Lys	Val	325	330	335	
Pro	Val	Tyr	Phe	Thr	Gly	Lys	Asp	Gly	Tyr	Glu	Thr	Lys	Asp	Leu	Thr	340	345	350	
Val	Glu	Trp	Glu	Glu	Val	Pro	Ala	Glu	Asn	Leu	Thr	Lys	Ala	Gly	Gln	355	360	365	
Phe	Thr	Val	Arg	Gly	Arg	Val	Leu	Gly	Ser	Asn	Leu	Val	Ala	Glu	Ile	370	375	380	
Thr	Val	Arg	Val	Thr	Asp	Lys	Leu	Gly	Glu	Thr	Leu	Ser	Asp	Asn	Pro	385	390	395	400
Asn	Tyr	Asp	Glu	Asn	Ser	Asn	Gln	Ala	Phe	Ala	Ser	Ala	Thr	Asn	Asp	405	410	415	
Ile	Asp	Lys	Asn	Ser	His	Asp	Arg	Val	Asp	Tyr	Leu	Asn	Asp	Gly	Asp	420	425	430	
His	Ser	Glu	Asn	Arg	Arg	Trp	Thr	Asn	Trp	Ser	Pro	Thr	Pro	Ser	Ser	435	440	445	
Asn	Pro	Glu	Val	Ser	Ala	Gly	Val	Ile	Phe	Arg	Glu	Asn	Gly	Lys	Ile	450	455	460	
Val	Glu	Arg	Thr	Val	Thr	Gln	Gly	Lys	Val	Gln	Phe	Phe	Ala	Asp	Ser	465	470	475	480
Gly	Thr	Asp	Ala	Pro	Ser	Lys	Leu	Val	Leu	Glu	Arg	Tyr	Val	Gly	Pro	485	490	495	
Glu	Phe	Glu	Val	Pro	Thr	Tyr	Tyr	Ser	Asn	Tyr	Gln	Ala	Tyr	Asp	Ala	500	505	510	
Asp	His	Pro	Phe	Asn	Asn	Pro	Glu	Asn	Trp	Glu	Ala	Val	Pro	Tyr	Arg	515	520	525	
Ala	Asp	Lys	Asp	Ile	Ala	Ala	Gly	Asp	Glu	Ile	Asn	Val	Thr	Phe	Lys	530	535	540	
Ala	Ile	Lys	Ala	Lys	Ala	Met	Arg	Trp	Arg	Met	Glu	Arg	Lys	Ala	Asp	545	550	555	560

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T022F0 2229260

Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu  
565 570 575

Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu  
580 585 590

Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys  
595 600 605

Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser  
610 615 620

Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu  
625 630 635 640

Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr  
645 650 655

Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp  
660 665 670

Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val  
675 680 685

Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln  
690 695 700

Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp  
705 710 715 720

Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp  
725 730 735

Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys  
740 745 750

Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu  
755 760 765

Ala Ser Gln Thr Asn Lys Ala Gln  
770 775

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTAA TTCAGACAGG	60
AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAGATC AGTTGCCTCA	120
AACAGGGACA GAA	133

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

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Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1           5           10           15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
20           25           30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
35           40

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(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA      60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAAATAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT          775

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(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 258 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn  
 1 5 10 15  
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr  
 20 25 30  
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp  
 35 40 45  
 Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro  
 50 55 60  
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu  
 65 70 75 80  
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu  
 85 90 95  
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp  
 100 105 110  
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu  
 115 120 125  
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp  
 130 135 140  
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln  
 145 150 155 160  
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr  
 165 170 175  
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala  
 180 185 190  
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys  
 195 200 205  
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys  
 210 215 220  
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys  
 225 230 235 240  
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr  
 245 250 255  
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

0976527E.012201

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GGATGCTCAA	GAAACTGCGG	GAGTTCAC	TAAATATGTG	GCAGATTTCAG	AGCTATCATC	60
AGAAGAAAAG	AAGCAGCTTG	TCTATGATAT	TCCGACATAC	GTGGAGAATG	ATGATGAAAC	120
TTATTATCTT	GTTTATAAGT	TAAATTCTCA	AAATCAACTG	GCGGAATTGC	CAAATACTGG	180
AAGCAAGAAT	GAGAGGCAA					199

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CGACAAAGGT	GAGACTGAGG	TTCAACCAGA	GTGCGCCAGAT	ACTGTGGTAA	GTGATAAAGG	60
TGAACCAGAG	CAGGTAGCAC	CGCTTCCAGA	ATATAAGGGT	AATATTGAGC	AAGTAAAACC	120
TGAAACTCCG	GTTGAGAAGA	CCAAAGAACA	AGGTCCAGAA	AAAACTGAAG	AAGTTCCAGT	180
AAAACCAACA	GAAGAAACAC	CAGTAAATCC	AAATGAAGGT	ACTACAGAAG	GAACCTCAAT	240

TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300  
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTCGAC 360  
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420  
 AAAAACTGTA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480  
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAT 540  
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600  
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660  
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720  
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAATGA 780  
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Lys	Gly	Glu	Thr	Glu	Val	Gln	Pro	Glu	Ser	Pro	Asp	Thr	Val	Val	1	5	10	15
Ser	Asp	Lys	Gly	Glu	Pro	Glu	Gln	Val	Ala	Pro	Leu	Pro	Glu	Tyr	Lys	20	25	30	
Gly	Asn	Ile	Glu	Gln	Val	Lys	Pro	Glu	Thr	Pro	Val	Glu	Lys	Thr	Lys	35	40	45	
Glu	Gln	Gly	Pro	Glu	Lys	Thr	Glu	Glu	Val	Pro	Val	Lys	Pro	Thr	Glu	50	55	60	
Glu	Thr	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Thr	Glu	Gly	Thr	Ser	Ile	65	70	75	80
Gln	Glu	Ala	Glu	Asn	Pro	Val	Gln	Pro	Ala	Glu	Glu	Ser	Thr	Thr	Asn	85	90	95	
Ser	Glu	Lys	Val	Ser	Pro	Asp	Thr	Ser	Ser	Lys	Asn	Thr	Gly	Glu	Val	100	105	110	
Ser	Ser	Asn	Pro	Ser	Asp	Ser	Thr	Thr	Ser	Val	Gly	Glu	Ser	Asn	Lys	115	120	125	
Pro	Glu	His	Asn	Asp	Ser	Lys	Asn	Glu	Asn	Ser	Glu	Lys	Thr	Val	Glu	130	135	140	
Glu	Val	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Val	Glu	Gly	Thr	Ser	Asn	145	150	155	160

Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn  
165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro  
180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn  
195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn  
210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val  
225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys  
245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys  
260 265 270

Thr Leu Glu Leu Arg Asn  
275

## (2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 709 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA	60
ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA	120
TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC	180
AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC	240
GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC	300
TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG	360
CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG	420
TTCACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC	480
TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCGCT	540
TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT	600
CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT	660
GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT	709

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu
1           5           10           15

Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val
          20           25           30

Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile
          35           40           45

Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala
          50           55           60

Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr
65           70           75           80

Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val
          85           90           95

Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly
          100          105          110

Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly
          115          120          125

Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser
          130          135          140

Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala
145          150          155          160

Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys
          165          170          175

Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val
          180          185          190

Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr
          195          200          205

Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala
210          215          220

Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn
225          230          235

```

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09765272.012204

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTACGA GAAAATGGCT CTGGGACACG 60  
GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120  
CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180  
GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240  
AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300  
ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360  
CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420  
AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTT 480  
CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540  
AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600  
AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAATCCTT GAAGAAGGTA AGAGTCTCAC 660  
CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTTGTGGTC AATAATGACA ATAAGGCAAG 720  
CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780  
GATTAAA 787

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly  
1 5 10 15  
Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys  
20 25 30  
Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln  
35 40 45  
Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala  
50 55 60  
Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu  
65 70 75 80  
Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu  
85 90 95

214

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser  
100 105 110

Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln  
115 120 125

Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr  
130 135 140

Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser  
145 150 155 160

Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys  
165 170 175

Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala  
180 185 190

Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser  
195 200 205

Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile  
210 215 220

Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser  
225 230 235 240

Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr  
245 250 255

Thr Trp Asp Lys Ile Lys  
260

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG	60
TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA	120
ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA	180
TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA	240
TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACACC AAGAGTCTCC TTAAGGCAGG	300
CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT	360
ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT	420
G	421

(2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1          5          10          15

Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
          20          25          30

Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
          35          40          45

Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
          50          55          60

Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65          70          75          80

Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
          85          90          95

Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
          100         105         110

Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
          115         120         125

Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
          130         135         140

```

## (2) INFORMATION FOR SEQ ID NO: 101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                     331

```

## (2) INFORMATION FOR SEQ ID NO:102:

09765272.012204

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1           5           10           15

Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
          20           25           30

Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
          35           40           45

Glu Ala Lys Lys Lys Val Glu Ala Glu Lys Lys Ala Lys Asp Gln
          50           55           60

Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65           70           75           80

Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
          85           90           95

Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC      60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC      120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA      180
TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA      240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT      300
TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT      358

```

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

09765373 013001

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Trp Thr Thr Gly Asn Trp Asp Glu Val Ile Ser Gly Lys Ile Asp Lys
1           5           10           15
Tyr Lys Asp Pro Asp Ile Pro Thr Val Glu Ser Gln Glu Val Thr Ser
20           25           30
Asp Ser Ser Asp Lys Glu Ile Thr Val Arg Tyr Asp Arg Leu Ser Thr
35           40           45
Pro Glu Lys Pro Ile Pro Gln Pro Asn Pro Glu His Pro Ser Val Pro
50           55           60
Thr Pro Asn Pro Glu Leu Pro Asn Gln Glu Thr Pro Thr Pro Asp Lys
65           70           75           80
Pro Thr Pro Glu Pro Gly Thr Pro Lys Thr Glu Thr Pro Val Asn Pro
85           90           95
Asp Pro Glu Val Pro Thr Tyr Glu Thr Gly Lys Arg Glu Glu Leu Pro
100          105          110
Asn Thr Gly Thr Glu Ala Asn
115

```

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1879 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA      60
GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT      120
TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC      180
AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA      240
GCTAACAGAT GTCTTAAAG AACTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG      300
TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG      360
CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG      420
TGTAACCAA GTAATTCCTT ATGAATATT CGCTGGTGAT GGTATGTAA CTCGTCTATT      480
ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT      540
ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA      600

```

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660  
TTATAAAGCT ACTGTTAAAG TTTACGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720  
AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780  
AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840  
AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900  
CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960  
AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020  
AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAACAAGC 1080  
GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140  
TG GTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200  
TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260  
NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320  
AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTGACTCG 1380  
TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTAAAAACCC 1440  
AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500  
CTTGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560  
CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620  
CTTGACAAC ATCGTAGCAA CTAAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680  
AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740  
TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800  
CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860  
GTCAGAGGAT AAAGCTATG 1879

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser  
1 5 10 15  
Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu  
20 25 30

Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro  
 35 40 45  
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser  
 50 55 60  
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu  
 65 70 75 80  
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly  
 85 90 95  
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly  
 100 105 110  
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu  
 115 120 125  
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val  
 130 135 140  
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu  
 145 150 155 160  
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys  
 165 170 175  
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe  
 180 185 190  
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala  
 195 200 205  
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr  
 210 215 220  
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu  
 225 230 235 240  
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys  
 245 250 255  
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp  
 260 265 270  
 Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr  
 275 280 285  
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly  
 290 295 300  
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser  
 305 310 315 320  
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn  
 325 330 335  
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn  
 340 345 350  
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa  
 355 360 365

09765522 042201  
 102270 22259260

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp  
 370 375 380  
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile  
 385 390 395 400  
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala  
 405 410 415  
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys  
 420 425 430  
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro  
 435 440 445  
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys  
 450 455 460  
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro  
 465 470 475 480  
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe  
 485 490 495  
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala  
 500 505 510  
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr  
 515 520 525  
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile  
 530 535 540  
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser  
 545 550 555 560  
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val  
 565 570 575  
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro  
 580 585 590  
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met  
 595 600 605  
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys  
 610 615 620  
 Ala Met  
 625

## (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 593 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60  
 TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120  
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180  
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240  
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300  
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360  
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420  
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480  
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540  
 CTTTGTGACT CAACACGCag CCTTTAACTa TCTTGCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser	Asn	Gln	Lys	Gln	Ala	Asp	Gly	Lys	Leu	Asn	Ile	Val	Thr	Thr	Phe	1	5	10	15
Tyr	Pro	Val	Tyr	Glu	Phe	Thr	Lys	Gln	Val	Ala	Gly	Asp	Thr	Ala	Asn	20	25	30	
Val	Glu	Leu	Leu	Ile	Gly	Ala	Gly	Thr	Glu	Pro	His	Glu	Tyr	Glu	Pro	35	40	45	
Ser	Ala	Lys	Ala	Val	Ala	Lys	Ile	Gln	Asp	Ala	Asp	Thr	Phe	Val	Tyr	50	55	60	
Glu	Asn	Glu	Asn	Met	Glu	Thr	Trp	Val	Pro	Lys	Leu	Leu	Asp	Thr	Leu	65	70	75	80
Asp	Lys	Lys	Lys	Val	Lys	Thr	Ile	Lys	Ala	Thr	Gly	Asp	Met	Leu	Leu	85	90	95	
Leu	Pro	Gly	Gly	Glu	Glu	Glu	Gly	Asp	His	Asp	His	Gly	Glu	Glu	100	105	110		
Gly	His	His	His	Glu	Phe	Asp	Pro	His	Val	Trp	Leu	Ser	Pro	Val	Arg	115	120	125	
Ala	Ile	Lys	Leu	Val	Glu	His	His	Pro	Arg	His	Leu	Ser	Ala	Asp	Tyr	130	135	140	
Pro	Asp	Lys	Lys	Glu	Thr	Phe	Glu	Lys	Asn	Ala	Ala	Ala	Tyr	Ile	Glu	145	150	155	160

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Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala  
 165 170 175

Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala  
 180 185 190

Leu Asp Tyr Gly Thr  
 195

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA TCGAACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGACTGC	60
TGCTGGCCAA CATGGTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTGCTCA	120
AATAGCATCA GATAAGGACA CGCTTGTTAT GGAACTTTCT TCTTTCCAAC TCATGGGTGT	180
TCAAGAAATC CATCCAGAGA TTGCGGTTAT TACCAACCTC ATGCCAACTC ATATCGACTA	240
CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGAAT ATCCAGAACA AGATGACAGC	300
AGCTGATTTC CTTGTCTTGA ACTTTAATCA AGACTTGGCA AAAGACTTGA CTTCCAAGAC	360
AGAAGCCACT GTTGTACCAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA	420
TGGTCAACTC TACTTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTTCCAGG	480
TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA	540
CAATCAAACC ATCAAGGAAA CTCTTTCAGC CTTCGGTGGT GTCAAACACC GTCTCCAGTT	600
TGTGGATGAC ATCAAGGGTG TTAAATTCTA TAACGACAGT AAATCAACTA ATATCTTGCC	660
TACTCAAAA GCCTTGTCAG GATTTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGGTTT	720
GGACCGTGGC AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT	780
CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA	840
TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG	900
AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT	960
ACGTGGCGAC CTCTTTATCG ACACAGTAGC GGAGTTAAAA GAA	1003

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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{xi} SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly	Ile	Thr	Gly	Ser	Asn	Gly	Lys	Thr	Thr	Thr	Thr	Met	Ile	Gly	1	5	10	15
Glu	Val	Leu	Thr	Ala	Ala	Gly	Gln	His	Gly	Leu	Leu	Ser	Gly	Asn	Ile	20	25	30
Gly	Tyr	Pro	Ala	Ser	Gln	Val	Ala	Gln	Ile	Ala	Ser	Asp	Lys	Asp	Thr	35	40	45
Leu	Val	Met	Glu	Leu	Ser	Ser	Phe	Gln	Leu	Met	Gly	Val	Gln	Glu	Phe	50	55	60
His	Pro	Glu	Ile	Ala	Val	Ile	Thr	Asn	Leu	Met	Pro	Thr	His	Ile	Asp	65	70	75
Tyr	His	Gly	Ser	Phe	Ser	Glu	Tyr	Val	Ala	Ala	Lys	Trp	Asn	Ile	Gln	85	90	95
Asn	Lys	Met	Thr	Ala	Ala	Asp	Phe	Leu	Val	Leu	Asn	Phe	Asn	Gln	Asp	100	105	110
Leu	Ala	Lys	Asp	Leu	Thr	Ser	Lys	Thr	Glu	Ala	Thr	Val	Val	Pro	Phe	115	120	125
Ser	Thr	Leu	Glu	Lys	Val	Asp	Gly	Ala	Tyr	Leu	Glu	Asp	Gly	Gln	Leu	130	135	140
Tyr	Phe	Arg	Gly	Glu	Val	Val	Met	Ala	Ala	Asn	Glu	Ile	Gly	Val	Pro	145	150	155
Gly	Ser	His	Asn	Val	Glu	Asn	Ala	Leu	Ala	Thr	Ile	Ala	Val	Ala	Lys	165	170	175
Leu	Arg	Asp	Val	Asp	Asn	Gln	Thr	Ile	Lys	Glu	Thr	Leu	Ser	Ala	Phe	180	185	190
Gly	Gly	Val	Lys	His	Arg	Leu	Gln	Phe	Val	Asp	Asp	Ile	Lys	Gly	Val	195	200	205
Lys	Phe	Tyr	Asn	Asp	Ser	Lys	Ser	Thr	Asn	Ile	Leu	Ala	Thr	Gln	Lys	210	215	220
Ala	Leu	Ser	Gly	Phe	Asp	Asn	Ser	Lys	Val	Val	Leu	Ile	Ala	Gly	Gly	225	230	235
Leu	Asp	Arg	Gly	Asn	Glu	Phe	Asp	Glu	Leu	Val	Pro	Asp	Ile	Thr	Gly	245	250	255
Leu	Lys	Lys	Met	Val	Ile	Leu	Gly	Gln	Ser	Ala	Glu	Arg	Val	Lys	Arg	260	265	270
Ala	Ala	Asp	Lys	Ala	Gly	Val	Ala	Tyr	Val	Glu	Ala	Thr	Asp	Ile	Ala	275	280	285
Asp	Ala	Thr	Arg	Lys	Ala	Tyr	Glu	Leu	Ala	Thr	Gln	Gly	Asp	Val	Val	290	295	300
Leu	Leu	Ser	Pro	Ala	Asn	Ala	Ser	Trp	Asp	Met	Tyr	Ala	Asn	Phe	Glu			

Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu  
325 330 335

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG	AAGATGGTTG	GGAAGTCCAC	TATATCGGGG	ACAAGTGTGG	TATCGAACAC	60
CAAGAAATCC	TTAAGTCAGG	TTTGGATGTC	ACCTTCCATT	CTATTGCGAC	TGGA <sup>1</sup> AAATTG	120
CGTCGCTATT	TCTCTTGGCA	AAATATGCTG	GACGTCTTCA	AAGTTGGTTG	GGGAATTGTC	180
CAATCGCTCT	TTATCATGTT	GCGACTGCGT	CCACAGACCC	TTTTTTCAA	GGGGGGCTTT	240
GTCTCAGTAC	CGCCTGTTAT	CGCTGCGCGT	GTGTCAGGAG	TGCCTGTCTT	TATTACAGAA	300
TCTGACCTGT	CTATGGGCTT	GGCCAATAAA	ATCGCCTATA	AATTTGCGAC	TAAGATGTAT	360
TCAACCTTTG	AACAAGCTTC	GAGTTTGGCT	AAGGTTGAGC	ATGTGGGAGC	GG	412

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser	Ser	Ser	Lys	Met	Val	Gly	Lys	Ser	Thr	Ile	Ser	Gly	Thr	Ser	Val
1			5						10					15	
Val	Ser	Asn	Thr	Lys	Lys	Ser	Leu	Ser	Gln	Val	Trp	Met	Ser	Pro	Ser
			20					25					30		
Ile	Leu	Leu	Arg	Leu	Glu	Asn	Cys	Val	Ala	Ile	Ser	Leu	Gly	Lys	Ile
		35					40						45		
Cys	Trp	Thr	Ser	Ser	Lys	Leu	Val	Gly	Glu	Leu	Ser	Asn	Arg	Ser	Leu
	50					55					60				
Ser	Cys	Cys	Asp	Cys	Val	His	Arg	Pro	Phe	Phe	Gln	Arg	Gly	Ala	Leu
65					70					75					80
Ser	Gln	Tyr	Arg	Leu	Leu	Ser	Leu	Arg	Val	Cys	Gln	Glu	Cys	Leu	Ser
				85					90					95	
Leu	Phe	Thr	Asn	Leu	Thr	Cys	Leu	Trp	Ala	Trp	Pro	Ile	Lys	Ser	Pro

225

100

105

110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val  
 115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60  
 AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTAC CCAATGGGCT 120  
 GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180  
 TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240  
 AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG 300  
 AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG 360  
 TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGTC TTACCGGCAG TTATCACTCC 420  
 GTTTGATACA ATAATGAAGG TGACTACAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480  
 TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540  
 GAAT 544

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr  
 1 5 10 15  
 Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser  
 20 25 30  
 Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys  
 35 40 45  
 Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile

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(2) INFORMATION FOR SEQ ID NO: 115:

(A) LENGTH: 1267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GCACCAGATG	GGGCACAAGG	TTCAGGGATC	AGATGTTGAA	AAGTACTACT	TTACCCAACG	60
CGGTCTTGAG	CAGGCAGGAA	TTACCATTCT	TCCTTTTGAT	GAATAAAATC	TAGACGGTGA	120
TATGGAAATT	ATCGCTGGAA	ATGCCTTTCG	TCCAGATAAC	AACGTCGAAA	TTGCCTATGC	180
GGACCAAAAT	GGTATCAGCT	ACAAACGTTA	CCATGAGTTT	CTAGGTAGCT	TTATGCGTGA	240
CTTTGTTAGC	ATGGGAGTAG	CAGGAGCACA	TGGAAAAACT	TCAACGACAG	GTATGTTGTC	300
TCATGTCTTG	TCTCACATTA	CAGATACCAG	CTTCTTGATT	GGAGATGGGA	CAGGTCGTGG	360
TTCGGCCAAT	GCCAAATATT	TTGTCTTTGA	ATCTGACGAA	TATGAGCGTC	ACTTCATGCC	420
TTACCACCCA	GAATACTCTA	TTATCACCAA	CATTGACTTT	GACCATCCAG	ATTATTTTAC	480
AAGTCTCGAG	GATGTTTTTA	ATGCCTTTAA	CGACTATGCC	AAACAAATCA	CCAAGGGTCT	540
TTTTGTCTAT	GGTGAAGATG	CTGAATTGCG	TAAGATTACG	TCTGATGCAC	CAATTTATTA	600
TTATGGTTTT	GAAGCTGAAG	GCAATGACTT	TGTAGCTAGT	GATCTTCTTC	GTTCAATAAC	660
TGGTTCAACC	TTCACCGTTC	ATTTCCGTGG	ACAAAACCTG	GGGCAATTCC	ACATTCCAAC	720
CTTTGGTCGT	CACAAATATCA	TGAATGCGAC	AGCCGTTATT	GGTCTTCTTT	ACACAGCAGG	780

ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840  
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCACC ATCCAACAGA 900  
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960  
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020  
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080  
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140  
 TGTGAAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200  
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260  
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr	1	5	10	15
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe	20	25	30	
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala	35	40	45	
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly	50	55	60	
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp	65	70	75	80
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr	85	90	95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu	100	105	110	
Ile	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Ser	Ala	Asn	Ala	Lys	Tyr	Phe	Val	115	120	125	
Phe	Glu	Ser	Asp	Glu	Tyr	Glu	Arg	His	Phe	Met	Pro	Tyr	His	Pro	Glu	130	135	140	
Tyr	Ser	Ile	Ile	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro	Asp	Tyr	Phe	Thr	145	150	155	160
Ser	Leu	Glu	Asp	Val	Phe	Asn	Ala	Phe	Asn	Asp	Tyr	Ala	Lys	Gln	Ile				

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165	170	175
Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile		
180	185	190
Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn		
195	200	205
Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe		
210	215	220
Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr		
225	230	235
Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu		
245	250	255
Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr		
260	265	270
Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr		
275	280	285
Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr		
290	295	300
Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val		
305	310	315
Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe		
325	330	335
Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr		
340	345	350
Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu		
355	360	365
Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val		
370	375	380
Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala		
385	390	395
Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn		
405	410	415
Leu Thr Ser Asn Val Gln		
420		

## (2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3121 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT

GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGA TAGCAT	120
GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTGCGAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT	540
AGTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC	780
AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC	840
AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACC GGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC	960
GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA	1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCTG TAGAACTAA	1140
AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AAC TGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTC AAT TAGAGTATAA	1500
GAAAATAGAG ATTAAAGATA TTGATT CAGT AGAATTATAC GGTAAAGAAA ATGATCGTTA	1560
TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT	1620
GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA	1680
TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA	1740
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC	1800
ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC	1860
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG	1920

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAAACAAAA TCGTATGCCA TTTATGATTT 1980  
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 2040  
 TGTTCCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100  
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160  
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220  
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280  
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340  
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400  
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460  
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520  
 TGTTCATACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580  
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640  
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700  
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760  
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCCT ATGGTAACAA 2820  
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA 2880  
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940  
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAACAG 3000  
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060  
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120  
 C 3121

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30  
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser  
 35 40 45

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Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu  
 50 55 60  
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly  
 65 70 75 80  
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu  
 85 90 95  
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln  
 100 105 110  
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu  
 115 120 125  
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly  
 130 135 140  
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser  
 145 150 155 160  
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys  
 165 170 175  
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val  
 180 185 190  
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr  
 195 200 205  
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln  
 210 215 220  
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val  
 225 230 235 240  
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu  
 245 250 255  
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu  
 260 265 270  
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
 275 280 285  
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
 290 295 300  
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
 305 310 315 320  
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
 325 330 335  
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg  
 340 345 350  
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu  
 355 360 365  
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg  
 370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val  
 385 390 395 400  
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn  
 405 410 415  
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala  
 420 425 430  
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys  
 435 440 445  
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu  
 450 455 460  
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu  
 465 470 475 480  
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln  
 485 490 495  
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu  
 500 505 510  
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu  
 515 520 525  
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg  
 530 535 540  
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp  
 545 550 555 560  
 Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly  
 565 570 575  
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys  
 580 585 590  
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala  
 595 600 605  
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr  
 610 615 620  
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly  
 625 630 635 640  
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala  
 645 650 655  
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr  
 660 665 670  
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn  
 675 680 685  
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val  
 690 695 700  
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val  
 705 710 715 720

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Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys  
725 730 735

Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile  
740 745 750

Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val  
755 760 765

Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly  
770 775 780

Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val  
785 790 795 800

Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly  
805 810 815

Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser  
820 825 830

Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala  
835 840 845

Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala  
850 855 860

Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val  
865 870 875 880

Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu  
885 890 895

Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu  
900 905 910

Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe  
915 920 925

Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr  
930 935 940

Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp  
945 950 955 960

Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys  
965 970 975

Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr  
980 985 990

Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr  
995 1000 1005

Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr  
1010 1015 1020

Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn  
1025 1030 1035 1040

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT	60
GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGA CTAGCAT	120
GGGAGTTCAA TTGTTGCCCG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTGCGAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT	540
AGTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTTGGAAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC	780
AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC	840
AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGA ACTTCC	960
GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA	1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCTG TAGAAACTAA	1140
AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTC CAAT TAGAGTATAA	1500
GAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAGAAA ATGATCGTTA	1560
TCGTAGA	1567

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
1           5           10           15

Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
          20           25           30

His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
          35           40           45

Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
          50           55           60

Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
65           70           75           80

Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
          85           90           95

Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
          100          105          110

Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
          115          120          125

Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
          130          135          140

Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
145          150          155          160

Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
          165          170          175

Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
          180          185          190

Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
          195          200          205

Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
          210          215          220

Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
225          230          235          240

Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
          245          250          255

Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu

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236

260

265

270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg  
340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu  
355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg  
370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val  
385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn  
405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala  
420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys  
435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu  
450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu  
465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln  
485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu  
500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg  
515 520

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1561 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 120  
 TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 180  
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 240  
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 300  
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 360  
 TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 420  
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTGG ATATTAAAAC 480  
 TGTTTCTGCT GATAGTAAAG AAAATGTTCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 540  
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 600  
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 660  
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 720  
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 780  
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 840  
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 900  
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 960  
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 1020  
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 1080  
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 1140  
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 1200  
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA 1260  
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA 1320  
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 1380  
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 1440  
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 1500  
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 1560  
 C 1561

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	1	5	10	15
Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	20	25	30	
Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	35	40	45	
Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	50	55	60	
Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	65	70	75	80
Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	85	90	95	
Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	100	105	110	
Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	115	120	125	
Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	130	135	140	
Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	145	150	155	160
Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala	165	170	175	
Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly	180	185	190	
Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile	195	200	205	
Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys	Leu	Ile	Ala	Asn	His	Gln	Asp	Ser	210	215	220	
Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile	Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser	225	230	235	240
Ser	Arg	Val	Asn	Lys	Val	Arg	Val	Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala	245	250	255	
Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly	Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn	260	265	270	
Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val	Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly	275	280	285	
Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly	Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn	290	295	300	
Gly	Arg	Val	Asn	Asn	Val	Val	Ser	Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr	305	310	315	320

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Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser  
325 330 335

Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser  
340 345 350

Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr  
355 360 365

Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp  
370 375 380

Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser  
385 390 395 400

Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His  
405 410 415

Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu  
420 425 430

Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn  
435 440 445

Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn  
450 455 460

Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser  
465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro  
485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser  
500 505 510

Asp Leu Gln Asn Val Thr Leu Asn  
515 520

## (2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 850 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG	60
TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA	120
GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA	180
AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA	240
AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA	300
ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA	360

CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420  
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480  
 TACTTCAATT GATGAAAGTA TGCCTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540  
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTAACCTACCG 600  
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660  
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720  
 TGATTGGGAT CTTCCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780  
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT 840  
 CAAAAATCGT 850

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe	Gly	Phe	Glu	Gly	Ser	Lys	Arg	Gly	Gln	Phe	Ala	Val	Glu	Gly	Ile	1	5	10	15
Asn	Gln	Leu	Arg	Glu	His	Val	Asp	Thr	Leu	Leu	Ile	Ile	Ser	Asn	Asn	20	25	30	
Asn	Leu	Leu	Glu	Ile	Val	Asp	Lys	Lys	Thr	Pro	Leu	Leu	Glu	Ala	Leu	35	40	45	
Ser	Glu	Ala	Asp	Asn	Val	Leu	Arg	Gln	Gly	Val	Gln	Gly	Ile	Thr	Asp	50	55	60	
Leu	Ile	Thr	Asn	Pro	Gly	Leu	Ile	Asn	Leu	Asp	Phe	Ala	Asp	Val	Lys	65	70	75	80
Thr	Val	Met	Ala	Asn	Lys	Gly	Asn	Ala	Leu	Met	Gly	Ile	Gly	Ile	Gly	85	90	95	
Ser	Gly	Glu	Glu	Arg	Val	Val	Glu	Ala	Ala	Arg	Lys	Ala	Ile	Tyr	Ser	100	105	110	
Pro	Leu	Leu	Glu	Thr	Thr	Ile	Asp	Gly	Ala	Glu	Asp	Val	Ile	Val	Asn	115	120	125	
Val	Thr	Gly	Gly	Leu	Asp	Leu	Thr	Leu	Ile	Glu	Ala	Glu	Glu	Ala	Ser	130	135	140	
Gln	Ile	Val	Asn	Gln	Ala	Gly	Gln	Gly	Val	Asn	Ile	Trp	Leu	Gly		145	150	155	160
Thr	Ser	Ile	Asp	Glu	Ser	Met	Arg	Asp	Glu	Ile	Arg	Val	Thr	Val	Val	165	170	175	

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Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln  
180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser  
195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro  
210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly  
225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val  
245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp  
260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg  
275 280

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTATTAG CTGATTTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG	540
AGCTTGTTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA	600
AGGACAATA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC	660
AGAAGGGGAG TGGGATTTGA TTCCCTTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA	720
CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTTGGG CAGGTGCCTG ACTTAACTGG	900

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TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCCTCACA ACTGGTCCTA TCATTGGTTA 960  
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCCTCTAA ATTACCCAAT 1020  
 TGAAAACATAT GTCAAACGAG TAAAAAGCGA A 1051

## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His  
 1 5 10 15  
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp  
 20 25 30  
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly  
 35 40 45  
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln  
 50 55 60  
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp  
 65 70 75 80  
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu  
 85 90 95  
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala  
 100 105 110  
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala  
 115 120 125  
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu  
 130 135 140  
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro  
 145 150 155 160  
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile  
 165 170 175  
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr  
 180 185 190  
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu  
 195 200 205  
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp  
 210 215 220  
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His

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(2) INFORMATION FOR SEQ ID NO: 127:

(A) LENGTH: 352 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TAAGGTCAAA	AGTCAGACCG	CTAAGAAAGT	GCTAGAAAAG	ATTGGAGCTG	ACTCGGTTAT	60
CTCGCCAGAG	TATGAAATGG	GGCAGTCTCT	AGCACAGACC	ATTCTTTTCC	ATAATAGTGT	120
TGATGTCTTT	CAGTTGGATA	AAAATGTGTC	TATCGTGGAG	AFGAAAATTC	CTCAGTCTTG	180
GGCAGGTCAA	AGTCTGAGTA	AATTAGACCT	CCGTGGCAAA	TACAATCTGA	ATATTTTGGG	240
TTTCCGAGAG	CAGGAAAATT	CCCCATTGGA	TGTTGAATTT	GGACCAGATG	ACCTCTTGAA	300
AGCAGATACC	TATATTTTGG	CAGTCATCAA	CAACCAGTAT	TTGGATACCC	TA	352

(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala  
1 5 10 15

Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln  
                   20                  25                  30  
 Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn  
                   35                  40                  45  
 Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser  
                   50                  55                  60  
 Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly  
                   65                  70                  75                  80  
 Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp  
                   85                  90                  95  
 Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln  
                   100                  105                  110  
 Tyr Leu Asp Thr Leu  
                   115

## (2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA	60
TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT	120
GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG	180
TGCCTACTTG AAAATTCTTG AAAGTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT	240
GTCTTTG	247

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 82 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser  
 1                  5                  10                  15  
 Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His  
                   20                  25                  30  
 Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

35	40	45
Lys Val Val Asp Ser Asp Asp Trp Val Asp Pro Arg Ala Tyr Leu Lys		
50	55	60
Ile Leu Glu Thr Cys Arg Asn Leu Arg Ala Lys Val Lys Arg Trp Met		
65	70	75
		80
Ser Leu		

## (2) INFORMATION FOR SEQ ID NO: 131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT GCCAAATGGT GGGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA	60
ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC	120
TGAAAAAGCC TTA CTGATT TGCCTCTGT TGATATGGAA ACGGGTGAAA TTCTGACAGA	180
GGAAGCTGTT CAAAATCTTC CACCTATTCC AGAAGAAAAG TGGGTGGAAC CAGAAATCAT	240
CCTGCCTCAA GCTGAACTTA AATTCCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT	300
TCAGGTCGAT TTTTCAGCCA AAGAAGCCCT TGAATACAAA CTTCCAAGCT TACAATCTTT	360
TGCACCAGAT AAACCAAAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCAGAG AAAATATCAA	420
AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT	480
TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGGCTGTT GGTGTAAGGG TCAACCGCAT	540
TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC	600
ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGCCC AACTCCGATA TTGCCACTGT	660
ATCTTTCCGA GAACTATGGG AACAAATCGCA AACGAAAGCA GAAAATTTCT TGGAAATTC	720
TTTAGGGAAG GCTGTTAATG GAACCGCAAG AGCTTTTGAC CTTTCTAAAA TGCCCCACTT	780
GCTAGTTGCA GGTTCACCGG GTTCAGGGAA GTCAGTAGCA GTTAACGGCA TTATTGCTAG	840
CATTCTCATG AAGGCGAGAC CAGATCAAGT TAAATTTATG ATGGTCGATC CCAAGATGGT	900
TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCACG	960
CAAAGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAATG GAAAACCGTT ATGAACTCTT	1020
TGCCAAGGTG GGAGTTCGGA ATATTGCAGG TTTTAATGCC AAGGTAGAAG AGTTCAATTC	1080
CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCATTGTC GTGATTGTGG ATGAGTTGGC	1140
TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGCT ATCATCCGTC TTGGGCAGAA	1200

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GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260  
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320  
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380  
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440  
 TGACGATGTT GAGCGCATTG TGAACCTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500  
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560  
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620  
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680  
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740  
 ACAA 1744

## (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu  
 1 5 10 15  
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu  
 20 25 30  
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro  
 35 40 45  
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln  
 50 55 60  
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile  
 65 70 75 80  
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp  
 85 90 95  
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr  
 100 105 110  
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln  
 115 120 125  
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala  
 130 135 140  
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile  
 145 150 155 160

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Gly Pro Ser Val Thr Lys Tyr Glu Val Lys Pro Ala Val Gly Val Arg  
 165 170 175  
 Val Asn Arg Ile Ser Asn Leu Ser Asp Asp Leu Ala Leu Ala Leu Ala  
 180 185 190  
 Ala Lys Asp Val Arg Ile Glu Ala Pro Ile Pro Gly Lys Ser Leu Ile  
 195 200 205  
 Gly Ile Glu Val Pro Asn Ser Asp Ile Ala Thr Val Ser Phe Arg Glu  
 210 215 220  
 Leu Trp Glu Gln Ser Gln Thr Lys Ala Glu Asn Phe Leu Glu Ile Pro  
 225 230 235 240  
 Leu Gly Lys Ala Val Asn Gly Thr Ala Arg Ala Phe Asp Leu Ser Lys  
 245 250 255  
 Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly Lys Ser Val  
 260 265 270  
 Ala Val Asn Gly Ile Ile Ala Ser Ile Leu Met Lys Ala Arg Pro Asp  
 275 280 285  
 Gln Val Lys Phe Met Met Val Asp Pro Lys Met Val Glu Leu Ser Val  
 290 295 300  
 Tyr Asn Asp Ile Pro His Leu Leu Ile Pro Val Val Thr Asn Pro Arg  
 305 310 315 320  
 Lys Ala Ser Lys Ala Leu Gln Lys Val Val Asp Glu Met Glu Asn Arg  
 325 330 335  
 Tyr Glu Leu Phe Ala Lys Val Gly Val Arg Asn Ile Ala Gly Phe Asn  
 340 345 350  
 Ala Lys Val Glu Glu Phe Asn Ser Gln Ser Glu Tyr Lys Gln Ile Pro  
 355 360 365  
 Leu Pro Phe Ile Val Val Ile Val Asp Glu Leu Ala Asp Leu Met Met  
 370 375 380  
 Val Ala Ser Lys Glu Val Glu Asp Ala Ile Ile Arg Leu Gly Gln Lys  
 385 390 395 400  
 Ala Arg Ala Ala Gly Ile His Met Ile Leu Ala Thr Gln Arg Pro Ser  
 405 410 415  
 Val Asp Val Ile Ser Gly Leu Ile Lys Ala Asn Val Pro Ser Arg Val  
 420 425 430  
 Ala Phe Ala Val Ser Ser Gly Thr Asp Ser Arg Thr Ile Leu Asp Glu  
 435 440 445  
 Asn Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp Met Leu Phe Lys Pro  
 450 455 460  
 Ile Asp Glu Asn His Pro Val Arg Leu Gln Gly Ser Phe Ile Ser Asp  
 465 470 475 480  
 Asp Asp Val Glu Arg Ile Val Asn Phe Ile Lys Thr Gln Ala Asp Ala  
 485 490 495

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Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly  
                   500                                  505                                  510  
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala  
                   515                                  520                                  525  
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln  
                   530                                  535                                  540  
 Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu  
                   545                                  550                                  555                                  560  
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg  
                                   565                                  570                                  575  
 Lys Val Leu Gln Gln  
                                   580

## (2) INFORMATION FOR SEQ ID NO: 133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGACTGAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCTA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTG GACTGATGCG GAATTGGAGC GTTATGATTT	600
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAA	829

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu  
 1 5 10 15  
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr  
 20 25 30  
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu  
 35 40 45  
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr  
 50 55 60  
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His  
 65 70 75 80  
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln  
 85 90 95  
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala  
 100 105 110  
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile  
 115 120 125  
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu  
 130 135 140  
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr  
 145 150 155 160  
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln  
 165 170 175  
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp  
 180 185 190  
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln  
 195 200 205  
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu  
 210 215 220  
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys  
 225 230 235 240  
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu  
 245 250 255  
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly  
 260 265 270  
 Leu Leu Lys Lys  
 275

(2) INFORMATION FOR SEQ ID NO: 135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA      60
AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT      120
CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG      180
AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGAATTGATG GATATCACAG ACGAAAAGGC      240
TGTTCCACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTACTATCGC      300
TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCGA      360
AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTGTGAA AAACCAGCTC CAGAGGACGC      420
TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT      480
CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTACAGCTG ACAGATGCAA TCGACACCCT      540
CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GTCGTTACG ATGTCGGAGA      600
CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA      660
TGATTTGAAG AATTACCTCA TCCAATTGG AAAAGAATTG ACTGAGAAGG AA              712

```

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn
1           5           10           15
Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr
          20           25           30
Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu
          35           40           45
Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe
          50           55           60
Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala
          65           70           75           80

```

Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala  
85 90 95

Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr  
100 105 110

Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val  
115 120 125

Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu  
130 135 140

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu  
145 150 155 160

Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala  
165 170 175

Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys  
180 185 190

Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser  
195 200 205

Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn  
210 215 220

Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu  
225 230 235

## (2) INFORMATION FOR SEQ ID NO: 137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTGAAAGC 60

CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC 120

TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AACTGGATT GTCCCTATGT 180

CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA 240

CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300

AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCGAAGAC ATGCAGCGTG CTGGTCGCCT 360

GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTATCAAA GGCGGACATC TCAAAGGTGG 420

TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480

AACCTGTCAC ACCCATGGTA CT 502

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala	Gln	Asn	Thr	Arg	Gly	Val	Gln	Leu	Ile	Glu	His	Val	Ser	Pro	Gln	
1				5				10					15			
Met	Leu	Lys	Ala	Gln	Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	
			20					25					30			
Ala	Val	Lys	Thr	Gly	Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	
			35				40					45				
Gln	Pro	Tyr	Leu	Lys	Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	
			50			55					60					
Met	Val	Ala	Thr	Ser	Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	
65					70					75					80	
Tyr	Leu	Lys	Thr	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	
				85					90					95		
Leu	Pro	Glu	Ala	Glu	Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	
			100					105					110			
Asp	Met	Gln	Arg	Ala	Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	
			115				120					125				
Ser	Val	Val	Ile	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe	
			130			135					140					
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln	
145					150					155					160	
Thr	Cys	His	Thr	His	Gly	Thr										
					165											

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 805 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA	TTAGAAAAAG	ATAGCAAATC	AGACAAAGAA	CAAGTTGATA	AACTATTTGA	60
ATCATTTGAT	GCATCTTCAG	ATGAATCTAT	TTCTAAATTA	AAAGAACTAT	CTGAAACTTC	120
ACTTAAACC	GATGCAGGTA	AAGACTATCT	TAATAACAAA	GTCAAAGAAT	CATCTAAAGC	180
AATTGTAGAT	TTTCATTTGC	AAAAAGGTTT	GGCTTATGAT	GTAAAGATT	CAGATGACAA	240

ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT 300  
 TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTTG GAAGAACTC TTAAATCTCT 360  
 AAATGATCTT GTTGATAAAT ATCAAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA 420  
 AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG 480  
 TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC 540  
 TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA 600  
 TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC 660  
 AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720  
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGGA ACTTTGGTGG 780  
 CGGCATTGCA GAACCTAGTC AACGC 805

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile	Val	Gln	Leu	Glu	Lys	Asp	Ser	Lys	Ser	Asp	Lys	Glu	Gln	Val	Asp	1	5	10	15
Lys	Leu	Phe	Glu	Ser	Phe	Asp	Ala	Ser	Ser	Asp	Glu	Ser	Ile	Ser	Lys	20	25	30	
Leu	Lys	Glu	Leu	Ser	Glu	Thr	Ser	Leu	Lys	Thr	Asp	Ala	Gly	Lys	Asp	35	40	45	
Tyr	Leu	Asn	Asn	Lys	Val	Lys	Glu	Ser	Ser	Lys	Ala	Ile	Val	Asp	Phe	50	55	60	
His	Leu	Gln	Lys	Gly	Leu	Ala	Tyr	Asp	Val	Lys	Asp	Ser	Asp	Asp	Lys	65	70	75	80
Phe	Lys	Asp	Lys	Ala	Thr	Leu	Glu	Thr	Asn	Val	Lys	Glu	Ile	Thr	Lys	85	90	95	
Gln	Ile	Asp	Phe	Ile	Lys	Lys	Val	Asp	Glu	Thr	Phe	Lys	Gln	Glu	Asn	100	105	110	
Leu	Glu	Glu	Thr	Leu	Lys	Ser	Leu	Asn	Asp	Leu	Val	Asp	Lys	Tyr	Gln	115	120	125	
Lys	Gln	Ile	Glu	Leu	Leu	Lys	Lys	Glu	Glu	Glu	Lys	Ala	Ala	Glu	Lys	130	135	140	
Ala	Ala	Glu	Lys	Ala	Lys	Glu	Ser	Ser	Ser	Gln	Ser	Asn	Ser	Ser	Gly	145	150	155	160

Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp  
                                   165                                  170                                  175

Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly  
                                   180                                  185                                  190

Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser  
                                   195                                  200                                  205

Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr  
                                   210                                  215                                  220

Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys  
                                   225                                  230                                  235                                  240

Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly  
                                   245                                  250                                  255

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg  
                                   260                                  265

## (2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCTGACCAAG CAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT	60
GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAGTT	120
ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA	180
AAATGGAGGA GCAAATCGTA AAGTCAATGA T	211

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val	
1                                  5                                  10                                  15	
Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn	
20                                  25                                  30	
Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu	
35                                  40                                  45	

Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala  
 50 55 60

Asn Arg Lys Val Asn Asp  
 65 70

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT 60  
 TGAAGAACTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAAA AGACTAGTCT 120  
 GAACTTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT 180  
 TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC 240  
 TAAGGTTGAA TTTCAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG 300  
 AAAAATTAAA CGCATTAAGG AAACAAAAAA T 331

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe  
 1 5 10 15  
 Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val  
 20 25 30  
 Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser  
 35 40 45  
 Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser  
 50 55 60  
 Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala  
 65 70 75 80  
 Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr  
 85 90 95  
 Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn  
 100 105 110

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## (2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 196 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAATC TTGCAAAGG AAGAAGTCTT      60
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA    120
GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT    180
GGCAATCAAA GAGCCA                                     196

```

## (2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys
1           5           10           15
Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn
          20           25           30
Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys
          35           40           45
Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu
          50           55           60
Pro
65

```

## (2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147: - - - - -

```

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGAAC AACTTGAGGT      60

```

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AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120  
 TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180  
 TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240  
 TCAACTGGTT CGCTTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300  
 TGTGGAAAAA GAAAAAAGT 319

## (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp  
 1 5 10 15  
 Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly  
 20 25 30  
 Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys  
 35 40 45  
 Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr  
 50 55 60  
 Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn  
 65 70 75 80  
 Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu  
 85 90 95  
 Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser  
 100 105

## (2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT 60  
 TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTTAA 120  
 TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA 180  
 TAAGAGCCAA TATGAGTTTC TGTTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA 240

AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA 300  
GCCTGAAAAG AAAGAGAATT CA 322

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn	Arg	Gln	Val	Ala	His	Tyr	Gln	Asp	Tyr	Ala	Leu	Asn	Lys	Glu	Lys
1				5					10					15	
Leu	Val	Ala	Phe	Ala	Met	Ala	Lys	Arg	Thr	Lys	Asp	Lys	Val	Glu	Gln
		20					25						30		
Glu	Ser	Gly	Glu	Gln	Phe	Phe	Asn	Leu	Gly	Gln	Val	Ser	Tyr	Gln	Asn
		35					40					45			
Lys	Lys	Thr	Gly	Leu	Val	Thr	Arg	Val	Arg	Thr	Asp	Lys	Ser	Gln	Tyr
		50				55					60				
Glu	Phe	Leu	Phe	Pro	Ser	Val	Lys	Ile	Lys	Glu	Glu	Lys	Arg	Asp	Lys
65					70				75					80	
Lys	Glu	Glu	Val	Ala	Thr	Asp	Ser	Ser	Glu	Lys	Val	Glu	Lys	Lys	Lys
			85						90					95	
Ser	Glu	Glu	Lys	Pro	Glu	Lys	Lys	Glu	Asn	Ser					
			100					105							

## (2) INFORMATION FOR SEQ ID NO: 151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTCGGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCTTACCC	60
AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG	120
AGTGCTACAA GAGTTTGTTG GTTGGAAAAC ATTAGAGATT AAAACTAAAG ACAGTGTTGG	180
AAGAAAGTAC GGGGAAAAAC GTGAAGATTC AGAAGATAAA GAAGAGAAGC GTTATTATAC	240
GAAGTATTAC TTTAATCAAA ATCATTCTTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA	300
CTGGTATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAC TACCTTGGTG GTGAAAGACG	360

TCGGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420  
 GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTTCCT CAGGAGCAAT 480  
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540  
 TATGAAAACA GGTGCGCAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600  
 TATGGCAACT GGTGCGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660  
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720  
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780  
 TCGG 784

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val	Val	Gly	Trp	Gln	Tyr	Ile	Pro	Phe	Pro	Ser	Lys	Gly	Ser	Thr	Ile	1	5	10	15
Gly	Pro	Tyr	Pro	Asn	Gly	Ile	Arg	Leu	Glu	Gly	Phe	Pro	Lys	Ser	Glu	20	25	30	
Trp	Tyr	Tyr	Phe	Asp	Lys	Asn	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Trp	35	40	45	
Lys	Thr	Leu	Glu	Ile	Lys	Thr	Lys	Asp	Ser	Val	Gly	Arg	Lys	Tyr	Gly	50	55	60	
Glu	Lys	Arg	Glu	Asp	Ser	Glu	Asp	Lys	Glu	Glu	Lys	Arg	Tyr	Tyr	Thr	65	70	75	80
Asn	Tyr	Tyr	Phe	Asn	Gln	Asn	His	Ser	Leu	Glu	Thr	Gly	Trp	Leu	Tyr	85	90	95	
Asp	Gln	Ser	Asn	Trp	Tyr	Tyr	Leu	Ala	Lys	Thr	Glu	Ile	Asn	Gly	Glu	100	105	110	
Asn	Tyr	Leu	Gly	Gly	Glu	Arg	Arg	Ala	Gly	Trp	Ile	Asn	Asp	Asp	Ser	115	120	125	
Thr	Trp	Tyr	Tyr	Leu	Asp	Pro	Thr	Thr	Gly	Ile	Met	Gln	Thr	Gly	Trp	130	135	140	
Gln	Tyr	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met	145	150	155	160
Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Gly	Thr	Thr	Trp	Tyr	Tyr	Leu	Asp	His	165	170	175	
Pro	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Gln	Asn	Leu	Gly	Asn	Lys	Trp				

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	180		185		190
Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp					
195		200		205	
Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr					
210		215		220	
Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly					
225		230		235	240
Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn					
	245		250		255
Gly Glu Trp Val Arg					
260					

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1708 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTTG GGATAAGGAA TCTTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA	540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGTTT	600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

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TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080  
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140  
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200  
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260  
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320  
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTTTTAA 1380  
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCATA GTGCCCTAGA 1440  
 AAGTAACTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500  
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560  
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA 1620  
 CAAGGCTTCT GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680  
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala	Lys	Ser	Glu	Trp	Val	Glu	Asp	Lys	Gly	Ala	Phe	Tyr	Tyr	Leu	Asp
1				5					10					15	
Gln	Asp	Gly	Lys	Met	Lys	Arg	Asn	Ala	Trp	Val	Gly	Thr	Ser	Tyr	Val
			20					25					30		
Gly	Ala	Thr	Gly	Ala	Lys	Val	Ile	Glu	Asp	Trp	Val	Tyr	Asp	Ser	Gln
		35					40					45			
Tyr	Asp	Ala	Trp	Phe	Tyr	Ile	Lys	Ala	Asp	Gly	Gln	His	Ala	Glu	Lys
	50					55					60				
Glu	Trp	Leu	Gln	Ile	Lys	Gly	Lys	Asp	Tyr	Tyr	Phe	Lys	Ser	Gly	Gly
65					70					75				80	
Tyr	Leu	Leu	Thr	Ser	Gln	Trp	Ile	Asn	Gln	Ala	Tyr	Val	Asn	Ala	Ser
				85				90						95	
Gly	Ala	Lys	Val	Gln	Gln	Gly	Trp	Leu	Phe	Asp	Lys	Gln	Tyr	Gln	Ser
			100					105					110		
Trp	Phe	Tyr	Ile	Lys	Glu	Asn	Gly	Asn	Tyr	Ala	Asp	Lys	Glu	Trp	Ile
		115					120					125			
Phe	Glu	Asn	Gly	His	Tyr	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	Met	Ala
	130						135					140			

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Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe  
 145 150 155 160  
 Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln  
 165 170 175  
 Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp  
 180 185 190  
 Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile  
 195 200 205  
 Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr  
 210 215 220  
 Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys  
 225 230 235 240  
 Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu  
 245 250 255  
 Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly  
 260 265 270  
 Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly Ser  
 275 280 285  
 Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala Tyr  
 290 295 300  
 Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly Glu  
 305 310 315 320  
 Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys Asp  
 325 330 335  
 Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu Ser  
 340 345 350  
 Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys Asp  
 355 360 365  
 Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr Val  
 370 375 380  
 Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met Glu  
 385 390 395 400  
 Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly Phe  
 405 410 415  
 Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr Asn  
 420 425 430  
 Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile Asn  
 435 440 445  
 Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu Glu  
 450 455 460  
 His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu Glu  
 465 470 475 480

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(2) INFORMATION FOR SEO ID NO: 155:

(A) LENGTH: 946 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

ATTTGCAGAT	GATTCTGAAG	GATGGCAGTT	TGTCCAAGAA	AATGGTAGAA	CCTACTACAA	60
AAAGGGGGAT	CTAAAAGAAA	CCTACTGGAG	AGTGATAGAT	GGGAAGTACT	ATTATTTTGA	120
TCCTTTATCC	GGAGAGATGG	TTGTCTGGCTG	GCAATATATA	CCTGCTCCAC	ACAAGGGGGT	180
TACGATTGGT	CCTTCTCCAA	GAATAGAGAT	TGCTCTTAGA	CCAGATTGGT	TTTATTTTGG	240
TCAAGATGGT	GTATTACAAG	AATTTGTTGG	CAAGCAAGTT	TTAGAAGCAA	AAACTGCTAC	300
GAATACCAAC	AAACATCATG	GGGAAGAATA	TGATAGCCAA	GCAGAGAAAC	GAGTCTATTA	360
TTTTGAAGAT	CAGCGTAGTT	ATCATACTTT	AAAAACTGGT	TGGATTTATG	AAGAGGGTCA	420
TTGGTATTAT	TTACAGAAGG	ATGGTGGCTT	TGATTTCGCGC	ATCAACAGAT	TGACGGTTGG	480
AGAGCTAGCA	CGTGGTTGGG	TTAAGGATTA	CCCTCTTACG	TATGATGAAG	AGAAGCTAAA	540
AGCAGCTCCA	TGGTACTATC	TAAATCCAGC	AACTGGCATT	ATGCAAACAG	GTTGGCAATA	600
TCTAGGTAAT	AGATGGTACT	ACCTCCATTC	GTCAGGAGCT	ATGGCAACTG	GCTGGTATAA	660
GGAAGGCTCA	ACTTGGTACT	ATCTAGATGC	TGAAAATGGT	GATATGAGAA	CTGGCTGGCA	720
AAACCTTGGG	AACAAATGGT	ACTATCTCCG	TTCATCAGGA	GCTATGGCAA	CTGGTTGGTA	780
TCAGGAAAGT	TCGACTTGGT	ACTATCTAAA	TGCAAGTAAT	GGAGATATGA	AAACAGGCTG	840
GTTCCAAGTC	AATGGTAACT	GGTACTATGC	CTATGATTCA	GGTGCTTTAG	CTGTTAATAC	900
CACAGTAGGT	GGTTACTACT	TAAACTATAA	TGGTGAATGG	GTTAAG		946

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly
1           5           10           15

Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val
          20           25           30

Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val
          35           40           45

Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly
          50           55           60

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe
65           70           75           80

Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu
          85           90           95

Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp
          100          105          110

Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr
          115          120          125

His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr
          130          135          140

Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val
145          150          155          160

Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp
          165          170          175

Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr
          180          185          190

Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr
          195          200          205

Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser
          210          215          220

Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp
225          230          235          240

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
          245          250          255

Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala
          260          265          270

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Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp  
 275 280 285

Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly  
 290 295 300

Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAACTG AAGTAGCAAA AACTTCGCAG GATACAACGA CAGCTTCAAG	60
TAGTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA	120
TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAGGAT GATGGTTCTA AAGCTCAAAG	180
TGAATGGATT TTTGACAACT ACTATAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA	240
CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCAAAA	300
CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA	360
TGCTCATCAA GAATGGCAAT TGATTGGAAA TAAGTGGTAC TACTTCAAGA AGTGGGGTTA	420
CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA	480
AAATGAATGG CTSCATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA	540
CTTATGCTAA CCAAGAGTGG CAAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG	600
GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG	660
CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TGCGGCCTCT GGTGAGCTCA	720
AAGAAAAAAA AGATTTGAAT GTCGGCTGGG TTCACAGAGA TG GTAAGCGC TATTTCTTTA	780
ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC	840
ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA	900
TTGTTTCGTCT AGGTTATAGC GGTAAAGAAG ACAAGGAATT GGCGCATAAC ATTAAGGAGT	960
TAAACCGTCT GGGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG	1020
ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT	1080
CTTACCCTAT CTATTATGAT GTTGAGAATT GGAATATGT AAATAAGAGC AAGAGAGCTC	1140
CAAGTGATAC AGGCACTTGG GTTAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG	1200
CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAC	1260

ACCCAGATAT TTAAAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320  
 AAAACCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380  
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr	1	5	10	15
Thr	Ala	Ser	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln	20	25	30	
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp	35	40	45	
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe	50	55	60	
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr	65	70	75	80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	85	90	95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe	100	105	110	
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile	115	120	125	
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser	130	135	140	
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln	145	150	155	160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys	165	170	175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys	180	185	190	
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln	195	200	205	
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val	210	215	220	
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys				

00765372 013304

(2) INFORMATION FOR SEQ ID NO: 159:

(A) LENGTH: 1924 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAACTTTC 60

ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA 120

AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC 180  
TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT 240  
TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC 300  
TGACGCTGAA TATCAGAAAA AATTAACAGA GGTCTGACTCT AAAATAGAGA AGGCTAGGAA 360  
AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC 420  
AAATGCGTTG GCTGAGACTA AGAAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC 480  
TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCACTA GCGAAGAAAAG AAGTAGAGGC 540  
TAAGGAACTT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC 600  
TACTGCTCAA CATCAAGTAG ATAATTTGAA AAAACTTCTT GCTGGTGCGG ATCCTGATGA 660  
TGGCACAGAA GTTATAGAAG CTAAATTTAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA 720  
AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAAACTT CTTGACAGCC TTGATCCTGA 780  
AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAAGC 840  
TGATGAACTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATATT 900  
ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA 960  
AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCCC 1020  
TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC 1080  
ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA 1140  
ACCAGAGCAA CCAGCTCCAG CTCCAAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA 1200  
GCAACCAGCT AAGCCGGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC 1260  
TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC 1320  
AATGGCAATA GGTGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC 1380  
TATGGCAACA GGTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC 1440  
TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG 1500  
CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG 1560  
TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTTCATGG TATTACCTCA ACGCTAATGG 1620  
TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG 1680  
TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG 1740  
TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG 1800  
TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT 1860  
AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG 1920  
GGTT 1924

(2) INFORMATION FOR SEQ ID NO:160:

09765272.012001

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

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Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
1           5           10           15

Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
          20           25           30

Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
          35           40           45

Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys Arg Thr Glu Glu Lys Ala
          50           55           60

Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
65           70           75           80

Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
          85           90           95

Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp
          100          105          110

Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys
          115          120          125

Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala
          130          135          140

Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala
145          150          155          160

Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys
          165          170          175

Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile
          180          185          190

Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn
          195          200          205

Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val
          210          215          220

Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln
225          230          235          240

Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser
          245          250          255

Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu
          260          265          270

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0965273 013304  
 T02210 222960

Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala  
 275 280 285  
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala  
 290 295 300  
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys  
 305 310 315 320  
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn  
 325 330 335  
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro  
 340 345 350  
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro  
 355 360 365  
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro  
 370 375 380  
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu  
 385 390 395 400  
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu  
 405 410 415  
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp  
 420 425 430  
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn  
 435 440 445  
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly  
 450 455 460  
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala  
 465 470 475 480  
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val  
 485 490 495  
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser  
 500 505 510  
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln  
 515 520 525  
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr  
 530 535 540  
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly  
 545 550 555 560  
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu  
 565 570 575  
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr  
 580 585 590  
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe  
 595 600 605

09765272-012201

Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala  
610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp  
625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA	60
ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA	120
TCCTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT	180
CTATGGTTAC TTGTCTATTC CAAGTTTGGA AATCATGGAG CCGGTTTATT TGGGAGCAGA	240
TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG	300
TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTCCG	360
CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT	420
AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC	480
GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCTTA CCTTTAATAA	540
ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC	600
TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC	660
TCAATGGTTG	670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu	
1 - - - - - 5 10 15	
Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu	
20 25 30	

Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu  
           35                                  40                                  45  
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu  
           50                                  55                                  60  
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp  
           65                                  70                                  75                                  80  
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu  
                                   85                                  90                                  95  
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala  
                                   100                                  105                                  110  
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly  
                                   115                                  120                                  125  
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met  
           130                                  135                                  140  
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser  
           145                                  150                                  155                                  160  
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro  
                                   165                                  170                                  175  
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr  
                                   180                                  185                                  190  
 Gln Lys Ser Asp Pro Gln Thr Ala Val Ala Arg Val Ala Phe Thr  
                                   195                                  200                                  205  
 Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu  
           210                                  215                                  220

## (2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA	60
TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACTCGCC AATTTAATGC	120
TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCGT AGCCAGGAAG AAACGACCCG	180
TCAGTACCAA CTTCAAGCCC TTTCGAGCCA GATTAATCCA CATTTCTCTT ATAACACTTT	240
GGACACCATC ATCTGGATGG CTGAATTTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA	300
GTCCTTGGCA ACCTATTTCC GCTTGGCGCT CAATCAAGGC AAGGACTTGA TTTGTCTCTC	360
TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA	420

GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480  
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540  
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600  
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660  
 TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720  
 GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780  
 TAGC 784

## (2) INFORMATION FOR SEQ ID NO:164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser  
 1 5 10 15  
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg  
 20 25 30  
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu  
 35 40 45  
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu  
 50 55 60  
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu  
 65 70 75 80  
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val  
 85 90 95  
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln  
 100 105 110  
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln  
 115 120 125  
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu  
 130 135 140  
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val  
 145 150 155 160  
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys  
 165 170 175  
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly  
 180 185 190

Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly  
 195 200 205  
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn  
 210 215 220  
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys  
 225 230 235 240  
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn  
 245 250 255  
 Arg Ile Glu Thr Ser  
 260

## (2) INFORMATION FOR SEQ ID NO: 165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT	240
GGACAATGTC ATAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA	300
AAAACGATTA AATGAGCTGA TAGAT	325

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile	1 5 10 15
Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His	20 25 30
Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys	35 40 45
Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly	50 55 60

Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met  
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala  
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp  
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA	60
TTTGTAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA	120
ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC	180
AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC	238

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln	
1 5 10 15	
Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp	
20 25 30	
His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe	
35 40 45	
Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu	
50 55 60	
Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu	
65 70 75	

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 169:

CTACTATCAA	TCAAGTTCTT	CAGCCATTGA	GGCCACCATT	GAGGGCAACA	GCCAAACGAC	60
CATCAGCCAG	ACTAGCCACT	TTATTCAGTC	TTATATCAAA	AAACTAGAAA	CCACCTCGAC	120
TGGTTTGACC	CAGCAGACGG	ATGTTCTGGC	CTATGCTGAG	AATCCCAGTC	AAGACAAGGT	180
CGAGGGAATC	CGAGATTTGT	TTTGTACCAT	CTTGAAGTCA	GATAAGGACT	TGAAAACGT	240
TGTGCTGGTG	ACCAAATCTG	GTCAGGTCAT	TTCTACAGAT	GACAGTGTGC	AGATGAAAAC	300
TTCTCTGAT	ATGATGGCTG	AGGATTGGTA	CCAAAAGGCC	ATTCATCAGG	GAGCTATGCC	360
TGTTTTGACT	CCAGCTCGTA	AATCAGATAG	TCAGTGGGTC	ATTTCTGTCA	CTCAAGAACT	420
TGTTGATGCA	AAGGGAGCCA	ATCTTGGTGT	GCTTCGTTTG	GATATTTCTT	ATGAAACTCT	480
GGAAGCCTAT	CTCAATCAAC	TCCAGTTGGG	GCAGCAGGGC	TTTGCCTTCA	TTATCAATGA	540
AAACCATGAA	TTTGTCTACC	ATCCTCAACA	CACAGTTTAT	AGTTCGTCTA	GCAAAATGGA	600
GGCTATGAAA	CCCTACATCG	ATACAGGTCA	GGGTTATACT	CCTGGTCACA	AATCCTACGT	660
CAGTCAAGAG	AAGATTGCAG	GAAGTGATTG	GACGGTGCTT	GGCGTGTCAT	CATTGGAAAA	720
GTTAGACCAG	GTTTCGGAGTC	AG				742

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr	Tyr	Gln	Ser	Ser	Ser	Ser	Ala	Ile	Glu	Ala	Thr	Ile	Glu	Gly	Asn	
1				5					10					15		
Ser	Gln	Thr	Thr	Ile	Ser	Gln	Thr	Ser	His	Phe	Ile	Gln	Ser	Tyr	Ile	
			20					25					30			
Lys	Lys	Leu	Glu	Thr	Thr	Ser	Thr	Gly	Leu	Thr	Gln	Gln	Thr	Asp	Val	
		35					40					45				
Leu	Ala	Tyr	Ala	Glu	Asn	Pro	Ser	Gln	Asp	Lys	Val	Glu	Gly	Ile	Arg	
	50					55					60					
Asp	Leu	Phe	Leu	Thr	Ile	Leu	Lys	Ser	Asp	Lys	Asp	Leu	Lys	Thr	Val	
65					--70--					75					80	
Val	Leu	Val	Thr	Lys	Ser	Gly	Gln	Val	Ile	Ser	Thr	Asp	Asp	Ser	Val	
				85					90					95		

Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys  
 100 105 110  
 Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser  
 115 120 125  
 Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys  
 130 135 140  
 Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu  
 145 150 155 160  
 Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe  
 165 170 175  
 Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val  
 180 185 190  
 Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr  
 195 200 205  
 Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys  
 210 215 220  
 Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys  
 225 230 235 240  
 Leu Asp Gln Val Arg Ser Gln  
 245

## (2) INFORMATION FOR SEQ ID NO: 171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA 60  
 GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTGAGGCCT ATGGTCTTCG 120  
 TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGGTGCAGT TTGCGGCCAA 180  
 GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG 240  
 TGCTGGTGAG TGGTTCCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA 300  
 CCCAGCCTTG ATTATGATTG CAGTGAAGTA AGCACCAGGC CTTGAAATCC ACCTTTCTAC 360  
 CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG 420  
 TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA 480  
 TGTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC 540  
 TCTTTCAAAC CACATGAGTA TCGGTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG 600

TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660  
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720  
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACTA 780  
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840  
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGAAGGTTG CCCAACGTGA 900  
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960  
 TCGTAAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020  
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG 1080  
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA 1140  
 AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200  
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260  
 AACCAGCGTC ACAGTTCGTG CT 1282

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu  
 1 5 10 15  
 Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile  
 20 25 30  
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe  
 35 40 45  
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys  
 50 55 60  
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly  
 65 70 75 80  
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val  
 85 90 95  
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro  
 100 105 110  
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu  
 115 120 125  
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala  
 130 135 140

Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp  
 145 150 155 160  
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser  
 165 170 175  
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg  
 180 185 190  
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met  
 195 200 205  
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu  
 210 215 220  
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp  
 225 230 235 240  
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa  
 245 250 255  
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val  
 260 265 270  
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp  
 275 280 285  
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly  
 290 295 300  
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg  
 305 310 315 320  
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp  
 325 330 335  
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu  
 340 345 350  
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr  
 355 360 365  
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala  
 370 375 380  
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln  
 385 390 395 400  
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr  
 405 410 415  
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala  
 420 425

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

FOUO 22222222

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60  
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120  
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180  
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240  
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300  
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360  
 CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTAAACT 420  
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480  
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540  
 CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600  
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660  
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720  
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile  
 1 5 10 15  
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys  
 20 25 30  
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr  
 35 40 45  
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile  
 50 55 60  
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg  
 65 70 75 80  
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu  
 85 90 95  
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu  
 100 105 110

09765273 012301

(2) INFORMATION FOR SEQ ID NO: 175:

(A) LENGTH: 694 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AGTAAATGCG	CAATCAAATT	CATTAATATT	AATAGATGAA	CCTGAAATCT	CACTTCATCC	60	
GAGTGCAATC	TATAAATTTA	AAGAGTTTTT	ACTTCAAGAG	TGTTTAAATA	AAAAACATCA	120	
AATTATTATC	ACTACACATT	CTACACAACT	TATAAAAGAT	TTTCCTAGAG	AAGCCGTGAA	180	
ACTTTTAGTG	AAAAACGGAG	AAAAGGTAGA	TGTTATTGAA	AATATTGATT	ATCAGGATGC	240	
ATTTTTTGAA	TTAGGTGATG	TGTATCATT	C	TAGGAAGATG	ATTTATGTTG	AAGATAGACT	300
AGCTAAATAT	ATTCTAGAGT	TTGTTATCAC	TCATT	CAGGT	AGTGAGAATC	TTAAACAGAA	360
TTTAGTAGTG	AGATATATTC	CTGGTGGAGC	AAATCAAATA	ATTTGTAATA	ATATTTTAAA	420	
CTCATCGTAT	TTAGATTCCG	ATAACCATTA	TTTTTGGCTT	GATGGAGATC	AAAACACTAA	480	
TGTTAGTGAA	TCAAATAATT	TAATGAACTA	TCTTGAAAAT	GGTGTGTGTTA	TATCAGATAA	540	
AATTCCTGAA	TCAGATAATA	AAAATCTTGA	TGATATTATA	AAATTGATAA	NGGGATGTCC	600	

AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA 660

ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC 694

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val	Asn	Ala	Gln	Ser	Asn	Ser	Leu	Ile	Leu	Ile	Asp	Glu	Pro	Glu	Ile	1	5	10	15
Ser	Leu	His	Pro	Ser	Ala	Ile	Tyr	Lys	Phe	Lys	Glu	Phe	Leu	Leu	Gln	20	25	30	
Glu	Cys	Leu	Asn	Lys	Lys	His	Gln	Ile	Ile	Ile	Thr	Thr	His	Ser	Thr	35	40	45	
Gln	Leu	Ile	Lys	Asp	Phe	Pro	Arg	Glu	Ala	Val	Lys	Leu	Leu	Val	Lys	50	55	60	
Asn	Gly	Glu	Lys	Val	Asp	Val	Ile	Glu	Asn	Ile	Asp	Tyr	Gln	Asp	Ala	65	70	75	80
Phe	Phe	Glu	Leu	Gly	Asp	Val	Tyr	His	Ser	Arg	Lys	Met	Ile	Tyr	Val	85	90	95	
Glu	Asp	Arg	Leu	Ala	Lys	Tyr	Ile	Leu	Glu	Phe	Val	Ile	Thr	His	Ser	100	105	110	
Gly	Ser	Glu	Asn	Leu	Lys	Gln	Asn	Leu	Val	Val	Arg	Tyr	Ile	Pro	Gly	115	120	125	
Gly	Ala	Asn	Gln	Ile	Ile	Cys	Asn	Asn	Ile	Leu	Asn	Ser	Ser	Tyr	Leu	130	135	140	
Asp	Ser	Asp	Asn	His	Tyr	Phe	Trp	Leu	Asp	Gly	Asp	Gln	Asn	Thr	Asn	145	150	155	160
Val	Ser	Glu	Ser	Asn	Asn	Leu	Met	Asn	Tyr	Leu	Glu	Asn	Gly	Val	Val	165	170	175	
Ile	Ser	Asp	Lys	Ile	Pro	Glu	Ser	Asp	Asn	Lys	Asn	Leu	Asp	Asp	Ile	180	185	190	
Ile	Lys	Leu	Ile	Xaa	Gly	Cys	Pro	Ile	Lys	Phe	Asn	Val	Ser	Gly	Asn	195	200	205	
Lys	Gly	Gln	Lys	Asn	Asn	Ile	Glu	Leu	Ile	Ala	Lys	Gln	Arg	Ser	Phe	210	215	220	
Ile	Asp	Tyr	Trp	Ala	Lys	Tyr	225	230											

(2) INFORMATION FOR SEQ ID NO: 177:

"0123456789" 222210

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT      60
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA      120
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA      180
CACCATCAAT GATAATGCCT CTAGCATTCG GCAAGGCATT CAAACTCTGA CAGGCAATCT      240
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG      300
ACCTGCCTAT ATCGATTTTA TCGCCCCAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA      360
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGAAT AGGACTGGAA AGACTTATAG      420
TTATATTCAC CCCATTTCCA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAACTA      480
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC      540
AACATCTGGC                                     550

```

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met
1           5           10           15
Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu
20        25        30
Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val
35        40        45
Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp
50        55        60
Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu
65        70        75        80
Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala
85        90        95
Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys

```

284

100	105	110
Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala		
115	120	125
Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro		
130	135	140
Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr		
145	150	155
Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe		
165	170	175
Thr Leu Phe Ser Thr Ser Gly		
180		

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA	60
GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTTG CGCGACCCAG CAGAATTCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGGATTCT TGAAAGGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val	
1	15
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp	
20	30
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg	
35	45

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys  
50 55 60

Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr  
65 70 75 80

Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile  
85 90 95

Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG	60
CAGCCAGTCA AGTCAGAAAA GTGAAACTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG	120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG	180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT	240
CTTGATGAAG GATCCAAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG	300
TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC	360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA	420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA	480
TGTTTATGTC TTAAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC	540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC	600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC	660
AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA	720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA	780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG	840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT	900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAGT GGTCTACAG TTTCTACAAA	960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT	1020
AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT	1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC	1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCAAACAAT AGTCTAGCAA CACCTTCTCC	1200

(2) INFORMATION FOR SEQ ID NO:182:

(A) LENGTH: 447 amino acids

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

225                      230                      235                      240  
 Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser  
                                  245                      250                      255  
 Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys  
                                  260                      265                      270  
 Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His  
                                  275                      280                      285  
 Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile  
                                  290                      295                      300  
 Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn  
                                  305                      310                      315                      320  
 Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn  
                                  325                      330                      335  
 Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly  
                                  340                      345                      350  
 Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr  
                                  355                      360                      365  
 Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln  
                                  370                      375                      380  
 Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro  
                                  385                      390                      395                      400  
 Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp  
                                  405                      410                      415  
 Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly  
                                  420                      425                      430  
 Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys  
                                  435                      440                      445

## (2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 934 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCAC TTTACAGCTA TCTTGGTGGA TTCAACACTA AAGTTCTTCC	60
AACTCCAATG ATGAACATCA TCAACGGTGG TTCTCACTCT GACGCTCCAA TCGCTTTCCA	120
AGAGTTCATG ATCTTGCCAG TTGGTGCGCC AACATTTAAA GAAGCCCTTC GTTACGGTGC	180
TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGTTCGGAAA CTGCCGTAGG	240
TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAAGTGA GATGGTGTTG AAATATCCT	300

TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360  
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420  
 TGAAGGTGCT GCTGTTTCGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480  
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGTTGGAA 540  
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600  
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660  
 AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720  
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780  
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840  
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900  
 TCGTGGATTG AAATCATTCT ACAACCTTAA AAAA 934

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr  
 1 5 10 15  
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His  
 20 25 30  
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly  
 35 40 45  
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His  
 50 55 60  
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly  
 65 70 75 80  
 Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val  
 85 90 95  
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys  
 100 105 110  
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys  
 115 120 125  
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala  
 130 135 140  
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn

09765272.012201

(2) INFORMATION FOR SEQ ID NO: 185:

(A) LENGTH: 541 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TCGTATCTTT	TTTTGGAGCA	ATGTTGCGGT	AGAAGGACAT	TCCATGGATC	CGACCCTAGC	60
GGATGGCGAA	ATTCTCTTCG	TTGTAAAAACA	CCTTCCTATT	GACCGTTTTG	ATATCGTGGT	120
GGCCCCATGAG	GAAGATGGCA	ATAAGGACAT	CGTCAAGCGC	GTGATTGGAA	TGCCTGGCGA	180
CACCATTTCGT	TACGAAAATG	ATAAACTCTA	CATCAATGAC	AAAGAAACGG	ACGAGCCTTA	240
TCTAGCAGAC	TATATCAAAC	GCTTCAAGGA	TGACAAACTC	CAAAGCACTT	ACTCAGGCAA	300
GGGCTTTGAA	GGAAATAAAG	GAACTTTCTT	TAGAAGTATC	GCTCAAAAAG	CTCAAGCCTT	360
CACAGTTGAT	GTCAACTACA	ACACCAACTT	TAGCTTTACT	GTTCCAGAAG	GAGAATACCT	420
TCTCCTCGGA	GATGACCGCT	TGGTTTCGAG	CGACAGCCGC	CACGTAGGTA	CCTTCAAAGC	480
AAAAGATATC	ACAGGGGAAG	CTAAATTCCG	CTTATGGCCA	ATCACCCGTA	TCGGAACATT	540
T						541

## (2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp
1           5           10           15
Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro
          20           25           30
Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys
          35           40           45
Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr
          50           55           60
Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr
          65           70           75           80
Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr
          85           90           95
Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser
          100          105          110
Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr
          115          120          125
Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp
          130          135          140
Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala
          145          150          155          160
Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg
          165          170          175
Ile Gly Thr Phe
          180

```

## (2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA

```

GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC      120
AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG      180
GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT      240
TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAAGTC CTTGCCAAAG CCCAAACCT      300
TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA      360
ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG      400

```

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
1           5           10           15

Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
          20           25           30

Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
          35           40           45

Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
          50           55           60

Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
          65           70           75           80

Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
          85           90           95

Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
          100          105          110

Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
          115          120          125

Leu Asp Lys Leu Lys
          130

```

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60  
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120  
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTA CTCTCAGGC TATTCTCAGT CAGCCATCTT 180  
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240  
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300  
 GACTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCACTGCT 360  
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420  
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480  
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540  
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600  
 AACTCTTATC AATCTCCTTA TGCCTTTTTA TCCCATTAGC TCGGGAGATA TCTTGCTGGA 660  
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720  
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780  
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840  
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900  
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960  
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020  
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCAG CCATTTCAGGA 1080  
 TGCGGATTTA ATTCTTGTCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140  
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200  
 A 1201

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile  
 1 5 10 15  
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln  
 20 25 30

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Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His  
 35 40 45  
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr  
 50 55 60  
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu  
 65 70 75 80  
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val  
 85 90 95  
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro  
 100 105 110  
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala  
 115 120 125  
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu  
 130 135 140  
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile  
 145 150 155 160  
 Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile  
 165 170 175  
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val  
 180 185 190  
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg  
 195 200 205  
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile  
 210 215 220  
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu  
 225 230 235 240  
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe  
 245 250 255  
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Ala Lys Ala  
 260 265 270  
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr  
 275 280 285  
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu  
 290 295 300  
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu  
 305 310 315 320  
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln  
 325 330 335  
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala  
 340 345 350  
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val  
 355 360 365

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Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg  
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG	60
AAAAGCAGTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC	120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC	180
CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAAC	240
AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT	300
CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAAA AATAACAAG GAAATGATGT	360
GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTTGG AAGTGATTAA	420
CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA	480
CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA	540
TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA	600
TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC	660
CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG	720
TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAAGACA AATTTGAGTC	780
TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA	840
AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT	900
TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG	960
CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT	1020
AGATTATGTT GAT	1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

097030372 012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Arg	Asn	Ala	Gly	Gln	Thr	Asp	Ala	Ser	Gln	Ile	Glu	Lys	Ala	Ala	Val	1	5	10	15
Ser	Gln	Gly	Gly	Lys	Ala	Val	Lys	Lys	Thr	Glu	Ile	Ser	Lys	Asp	Ala	20	25	30	
Asp	Leu	His	Glu	Ile	Tyr	Leu	Ala	Gly	Gly	Cys	Phe	Trp	Gly	Val	Glu	35	40	45	
Glu	Tyr	Phe	Ser	Arg	Val	Pro	Gly	Val	Thr	Asp	Ala	Val	Ser	Gly	Tyr	50	55	60	
Ala	Asn	Gly	Arg	Gly	Glu	Thr	Thr	Lys	Tyr	Glu	Leu	Ile	Asn	Gln	Thr	65	70	75	80
Gly	His	Ala	Glu	Thr	Val	His	Val	Thr	Tyr	Asp	Ala	Lys	Gln	Ile	Ser	85	90	95	
Leu	Lys	Glu	Ile	Leu	Leu	His	Tyr	Phe	Arg	Ile	Ile	Asn	Pro	Thr	Ser	100	105	110	
Lys	Asn	Lys	Gln	Gly	Asn	Asp	Val	Gly	Thr	Gln	Tyr	Arg	Thr	Gly	Val	115	120	125	
Tyr	Tyr	Thr	Asp	Asp	Lys	Asp	Leu	Glu	Val	Ile	Asn	Gln	Val	Phe	Asp	130	135	140	
Glu	Val	Ala	Lys	Lys	Tyr	Asp	Gln	Pro	Leu	Ala	Val	Glu	Lys	Glu	Asn	145	150	155	160
Leu	Lys	Asn	Phe	Val	Val	Ala	Glu	Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	165	170	175	
Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His	Ile	Asn	Val	Asn	Gln	Ala	Ala	Tyr	180	185	190	
Pro	Val	Ile	Asp	Ala	Ser	Lys	Tyr	Pro	Lys	Pro	Ser	Asp	Glu	Glu	Leu	195	200	205	
Lys	Lys	Thr	Leu	Ser	Pro	Glu	Glu	Tyr	Ala	Val	Thr	Gln	Glu	Asn	Gln	210	215	220	
Thr	Glu	Arg	Ala	Phe	Ser	Asn	Arg	Tyr	Trp	Asp	Lys	Phe	Glu	Ser	Gly	225	230	235	240
Ile	Tyr	Val	Asp	Ile	Ala	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	245	250	255	
Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Thr	Gln	Pro	Ile	Ser	260	265	270	
Pro	Asp	Val	Val	Thr	Tyr	Lys	Glu	Asp	Lys	Ser	Tyr	Asn	Met	Thr	Arg	275	280	285	
Met	Glu	Val	Arg	Ser	Arg	Val	Gly	Asp	Ser	His	Leu	Gly	His	Val	Phe	290	295	300	
Thr	Asp	Gly	Pro	Gln	Asp	Lys	Gly	Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	305	310	315	320

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 "022210" 22597650

Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr  
 325 330 335

Ala Tyr Leu Leu Asp Tyr Val Asp  
 340

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA	60
GAGCATGCGC CTGATAAAAT AGTTTTAGAT CATGCTTTTCG GTCAAACATAT ATTAGATAAA	120
AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA	180
ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTA GTGCTGATAA AGGAGTTTTA	240
CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG	300
GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT	360
TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA	396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu	
1 5 10 15	
Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala	
20 25 30	
Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile	
35 40 45	
Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val	
50 55 60	
Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu	
65 70 75 80	
Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu	
85 90 95	

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Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys  
 100 105 110

Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr  
 115 120 125

Asp Thr Leu Ser  
 130

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAATATA GAAATTATTT TAGTTGATGA	60
CGGTTCTACG GATAATTCTG GGGAAATTTG TGATGCTTTT ATGATGCAAG ATAATCGTGT	120
GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG	180
TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTTCAGAT GATATCGTAA AAGAAAATAT	240
GATTGAAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA	300
CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTAT GTAACAGGGC AAGATTTTTG	360
CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA	420
TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT	480
TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT	540
AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG	600
CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTTTTCTAA	660
GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT	720
CAATCTTTTA AAAGATTATA AGCAAACCTT AGAATACCAT CAATTAACAG ATACTGAGGA	780
ATATAAAGAT ATTTGTTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA	840
AAGT	844

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 281 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09765272 012204

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile  
 1 5 10 15  
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala  
 20 25 30  
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys  
 35 40 45  
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly  
 50 55 60  
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met  
 65 70 75 80  
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val  
 85 90 95  
 Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe  
 100 105 110  
 Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu  
 115 120 125  
 Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe  
 130 135 140  
 Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val  
 145 150 155 160  
 His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg  
 165 170 175  
 Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr  
 180 185 190  
 Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu  
 195 200 205  
 Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp  
 210 215 220  
 Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val  
 225 230 235 240  
 Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr  
 245 250 255  
 Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe  
 260 265 270  
 Asp Ala Glu Gln Arg Asn Gly Lys Ser  
 275 280

## (2) INFORMATION FOR SEQ ID NO: 197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTTCAGA ATCAGACGTA TCAAAATTTT GAGTGTTTAT TAATCAATGA 60  
 TGGCTCTCCA GATCATTTCAT CCAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120  
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180  
 TTCGGGGGGG GCGTACATTA CTTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240  
 AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GGC GTTATAA 300  
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360  
 AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420  
 GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480  
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540  
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600  
 ATCGAATACA TGGAGTGAAG AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660  
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720  
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTTACAG 780  
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu  
 1 5 10 15  
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu  
 20 25 30  
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly  
 35 40 45  
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala  
 50 55 60  
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu  
 65 70 75 80  
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile  
 85 90 95

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr  
 100 105 110  
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile  
 115 120 125  
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val  
 130 135 140  
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe  
 145 150 155 160  
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu  
 165 170 175  
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr  
 180 185 190  
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg  
 195 200 205  
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala  
 210 215 220  
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg  
 225 230 235 240  
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr  
 245 250 255  
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro  
 260 265 270

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA 60  
 TGCTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT 120  
 TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA 180  
 TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT 240  
 AGAAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA 300  
 TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA 360  
 GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGTAT GAAACTCAAG AAATGAAGAG 420  
 TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG 480  
 CTTTGACATA GGTAAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC 540

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600  
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660  
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720  
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780  
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840  
 GAAAGCCATT GTCCTCGCAG CAAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA 900  
 GTCTATTTGT TATCATAATC GTTCGATTCTG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960  
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020  
 TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080  
 ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140  
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200  
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260  
 TCTCTGGTA AACAAATGCTT TTTGGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320  
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380  
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440  
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCATC ATCTTTCTCA 1500  
 TCGGAAACCG TGGAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560  
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620  
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680  
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTAAAGATAG CAGCTAGAGT 1740  
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800  
 AATTCATCTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860  
 TATTAATCAT GGCGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920  
 TATCTTATCC TTTGAAAATA CTAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980  
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val  
 1 5 10 15  
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu  
 20 25 30  
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala  
 35 40 45  
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn  
 50 55 60  
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val  
 65 70 75 80  
 Glu Thr Leu Tyr Lys Lys Ile Val Glu Tyr Gln Ala Asp Ile Ala Val  
 85 90 95  
 Gly Asn Tyr Tyr Ser Phe Asn Glu Ser Glu Gly Met Phe Tyr Phe His  
 100 105 110  
 Ile Leu Gly Asp Ser Tyr Tyr Glu Lys Val Tyr Asp Asn Val Ser Ile  
 115 120 125  
 Phe Glu Asn Leu Tyr Glu Thr Gln Glu Met Lys Ser Phe Ala Leu Ile  
 130 135 140  
 Ser Ala Trp Gly Lys Leu Tyr Lys Ala Arg Leu Phe Glu Gln Leu Arg  
 145 150 155 160  
 Phe Asp Ile Gly Lys Leu Gly Glu Asp Gly Tyr Leu Asn Gln Lys Val  
 165 170 175  
 Tyr Leu Leu Ser Glu Lys Val Ile Tyr Leu Asn Lys Ser Leu Tyr Ala  
 180 185 190  
 Tyr Arg Ile Arg Lys Gly Ser Leu Ser Arg Val Trp Thr Glu Lys Trp  
 195 200 205  
 Met His Ala Leu Val Asp Ala Met Ser Glu Arg Ile Thr Leu Leu Ala  
 210 215 220  
 Asn Met Gly Tyr Pro Leu Glu Lys His Leu Ala Val Tyr Arg Gln Met  
 225 230 235 240  
 Leu Glu Val Ser Leu Ala Asn Gly Gln Ala Ser Gly Leu Ser Asp Thr  
 245 250 255  
 Ala Thr Tyr Lys Glu Phe Glu Met Lys Gln Arg Leu Leu Asn Gln Leu  
 260 265 270  
 Ser Arg Gln Glu Glu Ser Glu Lys Lys Ala Ile Val Leu Ala Ala Asn  
 275 280 285  
 Tyr Gly Tyr Val Asp Gln Val Leu Thr Thr Ile Lys Ser Ile Cys Tyr  
 290 295 300  
 His Asn Arg Ser Ile Arg Phe Tyr Leu Ile His Ser Asp Phe Pro Asn  
 305 310 315 320  
 Glu Trp Ile Lys Gln Leu Asn Lys Arg Leu Glu Lys Phe Asp Ser Glu  
 325 330 335

00765373 012304

Ile Ile Asn Cys Arg Val Thr Ser Glu Gln Ile Ser Cys Tyr Lys Ser  
 340 345 350  
 Asp Ile Ser Tyr Thr Val Phe Leu Arg Tyr Phe Ile Ala Asp Phe Val  
 355 360 365  
 Gln Glu Asp Lys Ala Leu Tyr Leu Asp Cys Asp Leu Val Val Thr Lys  
 370 375 380  
 Asn Leu Asp Asp Leu Phe Ala Thr Asp Leu Gln Asp Tyr Pro Leu Ala  
 385 390 395 400  
 Ala Val Arg Asp Phe Gly Gly Arg Ala Tyr Phe Gly Gln Glu Ile Phe  
 405 410 415  
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn  
 420 425 430  
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val  
 435 440 445  
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp  
 450 455 460  
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe  
 465 470 475 480  
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His  
 485 490 495  
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr  
 500 505 510  
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly  
 515 520 525  
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile  
 530 535 540  
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu  
 545 550 555 560  
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile  
 565 570 575  
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr  
 580 585 590  
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp  
 595 600 605  
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly  
 610 615 620  
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro  
 625 630 635 640  
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala  
 645 650 655  
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile  
 660 665 670

056522 012201

Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 910 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA	60
TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA	120
TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG ATGAAGCAGG CTCACGGGGA	180
TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA	240
TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC	300
TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC	360
ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT	420
CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA	480
TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCTATTA	540
TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC	600
CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA	660
AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT	720
AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAGGCCA	780
TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC	840
CCTATTCATA AATATTTCTT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA	900
AAAATTACAT	910

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile	Gln	Lys	Gln	Thr	Tyr	Gln	Asn	Leu	Glu	Ile	Ile	Leu	Val	Asp	Asp
1				5				10						15	

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln  
                   20                                  25                                  30  
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln  
                   35                                  40                                  45  
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe  
                   50                                  55                                  60  
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr  
                   65                                  70                                  75                                  80  
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met  
                                   85                                  90                                  95  
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp  
                                   100                                  105                                  110  
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly  
                                   115                                  120                                  125  
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile  
                   130                                  135                                  140  
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr  
                   145                                  150                                  155                                  160  
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr  
                                   165                                  170                                  175  
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys  
                                   180                                  185                                  190  
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe  
                   195                                  200                                  205  
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe  
                   210                                  215                                  220  
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu  
                   225                                  230                                  235                                  240  
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe  
                                   245                                  250                                  255  
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys  
                                   260                                  265                                  270  
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr  
                   275                                  280                                  285  
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His  
                   290                                  295                                  300

## (2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1972 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT	60
TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG	120
AGCATGGGAA GCTATTCCTG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCCTGC	180
AAAAGTCTGT AAACCAACAA GTTGTATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA	240
TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC	300
GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG	360
TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC	420
GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA	480
TCATGAAAAA TGGTCTCGGG AAACATTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA	540
AAAATATCAT AAAAATTGG TGTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG	600
TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC	660
AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTGAAA CTGGAAGAGC	720
TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA	780
TGTATATACT GGGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC	840
AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTCTTTA GACATGCTAT	900
ACAAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAATAGA ACAAAGCTG TATTTTGGAA	960
TGGAGAAGGT AGGATTAGTT CATTAACGG ATTTTATCAA GGACTTTATT CGAATGATGA	1020
AACAATGCCT TTATATAATA ATGGGAGATA TCATATTCTT CCTGTAATAC ATGAGAAAAT	1080
TGATAAGGAA AAGATTTTAT CTATATTCCC TAATGCAAAA ATTTTGACTA AAAATAGTGA	1140
GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA	1200
TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA	1260
TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA	1320
TTTGACGCCA CATACTTACG CTGTTGTTAA AGAAAATCCA AATAATTTAC ATATTTTATT	1380
GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC	1440
AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT	1500
CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAAGGGC ATACTGGTCA	1560
TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA	1620
TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT	1680
AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA	1740
TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC	1800

(2) INFORMATION FOR SEQ ID NO:204:

(A) LENGTH: 657 amino acids

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Pro Leu Leu Leu Ser Pro Leu Tyr Gly Asn Asp Asn Gly Asn Gly Leu  
20 25 30

Trp Trp Gly Asn Thr Leu Lys Gly Ala Trp Glu Ala Ile Pro Glu Asp  
35 40 45

Val Lys Pro Tyr Ala Ala Ile Glu Leu His Pro Ala Lys Val Cys Lys  
50 55 60

Pro Thr Ser Cys Ile Pro Arg Asp Thr Lys Glu Leu Arg Glu Trp Tyr  
65 70 75 80

Val Lys Met Leu Glu Glu Ala Gln Ser Leu Asn Ile Pro Val Phe Leu  
85 90 95

Val Ile Met Ser Ala Gly Glu Arg Asn Thr Val Pro Pro Glu Trp Leu  
100 105 110

Asp Glu Gln Phe Gln Lys Tyr Ser Val Leu Lys Gly Val Leu Asn Ile  
115 120 125

Glu Asn Tyr Trp Ile Tyr Asn Asn Gln Leu Ala Pro His Ser Ala Lys  
130 135 140

Tyr Leu Glu Val Cys Ala Lys Tyr Gly Ala His Phe Ile Trp His Asp  
145 150 155 160

His Glu Lys Trp Phe Trp Glu Thr Ile Met Asn Asp Pro Thr Phe Phe  
165 170 175

Glu Ala Ser Gln Lys Tyr His Lys Asn Leu Val Leu Ala Thr Lys Asn  
180 185 190

Thr Pro Ile Arg Asp Asp Ala Gly Thr Asp Ser Ile Val Ser Gly Phe  
195 200 205

Trp Leu Ser Gly Leu Cys Asp Asn Trp Gly Ser Ser Thr Asp Thr Trp  
210 215 220

Lys Trp Trp Glu Lys His Tyr Thr Asn Thr Phe Glu Thr Gly Arg Ala

225                      230                      235                      240  
 Arg Asp Met Arg Ser Tyr Ala Ser Glu Pro Glu Ser Met Ile Ala Met  
                                  245                      250                      255  
 Glu Met Met Asn Val Tyr Thr Gly Gly Gly Thr Val Tyr Asn Phe Glu  
                                  260                      265                      270  
 Cys Ala Ala Tyr Thr Phe Met Thr Asn Asp Val Pro Thr Pro Ala Phe  
                                  275                      280                      285  
 Thr Lys Gly Ile Ile Pro Phe Phe Arg His Ala Ile Gln Asn Pro Ala  
                                  290                      295                      300  
 Pro Ser Lys Glu Glu Val Val Asn Arg Thr Lys Ala Val Phe Trp Asn  
 305                                   310                      315                      320  
 Gly Glu Gly Arg Ile Ser Ser Leu Asn Gly Phe Tyr Gln Gly Leu Tyr  
                                  325                      330                      335  
 Ser Asn Asp Glu Thr Met Pro Leu Tyr Asn Asn Gly Arg Tyr His Ile  
                                  340                      345                      350  
 Leu Pro Val Ile His Glu Lys Ile Asp Lys Glu Lys Ile Ser Ser Ile  
                                  355                      360                      365  
 Phe Pro Asn Ala Lys Ile Leu Thr Lys Asn Ser Glu Glu Leu Ser Ser  
                                  370                      375                      380  
 Lys Val Asn Tyr Leu Asn Ser Leu Tyr Pro Lys Leu Tyr Glu Gly Asp  
 385                                   390                      395                      400  
 Gly Tyr Ala Gln Arg Val Gly Asn Ser Trp Tyr Ile Tyr Asn Ser Asn  
                                  405                      410                      415  
 Ala Asn Ile Asn Lys Asn Gln Gln Val Met Leu Pro Met Tyr Thr Asn  
                                  420                      425                      430  
 Asn Thr Lys Ser Leu Ser Leu Asp Leu Thr Pro His Thr Tyr Ala Val  
                                  435                      440                      445  
 Val Lys Glu Asn Pro Asn Asn Leu His Ile Leu Leu Asn Asn Tyr Arg  
                                  450                      455                      460  
 Thr Asp Lys Thr Ala Met Trp Ala Leu Ser Gly Asn Phe Asp Ala Ser  
 465                                   470                      475                      480  
 Lys Ser Trp Lys Lys Glu Glu Leu Glu Leu Ala Asn Trp Ile Ser Lys  
                                  485                      490                      495  
 Asn Tyr Ser Ile Asn Pro Val Asp Asn Asp Phe Arg Thr Thr Thr Leu  
                                  500                      505                      510  
 Thr Leu Lys Gly His Thr Gly His Lys Pro Gln Ile Asn Ile Ser Gly  
                                  515                      520                      525  
 Asp Lys Asn His Tyr Thr Tyr Thr Glu Asn Trp Asp Glu Asn Thr His  
                                  530                      535                      540  
 Val Tyr Thr Ile Thr Val Asn His Asn Gly Met Val Glu Met Ser Ile  
 545                                   550                      555                      560  
 Asn Thr Glu Gly Thr Gly Pro Val Ser Phe Pro Thr Pro Asp Lys Phe

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565 570 575

Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser  
580 585 590

Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg  
595 600 605

Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn  
610 615 620

Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu  
625 630 635 640

Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn  
645 650 655

Phe

## (2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTTC	60
ACGAGAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAA ATCACAGGGA TTCTCAAAAA	120
AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA	180
AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC	240
TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT	300
TTTAGATGGT GAATACCCTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC	360
CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC	420
AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC	480
AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA	540
AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC	600
AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGAATTAAC	660
TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT	720
GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACTTGCAG ACGTTTTTAG	780
TGGCAAATTA ACCACCTGGG ACAAGATTAA A	811

## (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys	Gly	Asn	Gln	Ser	Ala	Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	1	5	10	15
Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	20	25	30	
Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	35	40	45	
Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	50	55	60	
Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	65	70	75	80
Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	85	90	95	
Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	100	105	110	
Ile	Val	Trp	Ser	Ser	Asn	Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	115	120	125	
Phe	Ile	His	Ser	Lys	Gln	Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	130	135	140	
Ile	Glu	Ala	Lys	Thr	Glu	Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	145	150	155	160
Gly	Lys	Leu	Ser	Val	Val	Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	165	170	175	
Lys	Leu	Ala	Glu	Ala	Tyr	Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	180	185	190	
Ile	Thr	Ser	Asn	Gly	Ser	Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	195	200	205	
Thr	Ala	Asp	Ile	Gly	Met	Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	210	215	220	
Lys	Ser	Leu	Thr	His	Asp	Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	225	230	235	240
Val	Asn	Asn	Asp	Asn	Lys	Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	245	250	255	
Asp	Val	Phe	Ser	Gly	Lys	Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys			260	265	270	

(2) INFORMATION FOR SEQ ID NO: 207:

09765372 013301

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60  
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120  
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTGAT GCATTTTTTA ATCTCGTTAA 180  
 TGACTATAAT ACCATTGTCT GCTCAACTGG CTTATCAGGA GATTTCACTT CCTTTACTCA 240  
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300  
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360  
 GCTTGAAAAG AATGACCACT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420  
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480  
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540  
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600  
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GCTTTCTTAT TTGTAGAGAA 660  
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720  
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTTATCAT 780  
 GGATAATGAT AAGTGGGTTA AACTT 805

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser  
 1 5 10 15  
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn  
 20 25 30  
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp  
 35 40 45  
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr  
 50 55 60

Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His  
 65 70 75 80  
 Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys  
 85 90 95  
 Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu  
 100 105 110  
 Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu  
 115 120 125  
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln  
 130 135 140  
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser  
 145 150 155 160  
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser  
 165 170 175  
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His  
 180 185 190  
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu  
 195 200 205  
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu  
 210 215 220  
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys  
 225 230 235 240  
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys  
 245 250 255  
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu  
 260 265

## (2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA	60
GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG	120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT	180
CTGGGCTTCT TGGTGTTCCT TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA	240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTCA CCAGGACATA AGGGAGAGCA	300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT	360

AGTTGACCCA TCAGGCAAAC TTTTGGAAAC TTATGGTGTG CGTTCCTTACC CAACCCAAGC 420  
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480  
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys	Ser	Gly	Lys	Ser	Val	Thr	Ser	Glu	His	Gln	Thr	Lys	Asp	Glu	Met
1			5						10					15	
Lys	Thr	Glu	Gln	Thr	Ala	Ser	Lys	Thr	Ser	Ala	Ala	Lys	Gly	Lys	Glu
		20						25					30		
Val	Ala	Asp	Phe	Glu	Leu	Met	Gly	Val	Asp	Gly	Lys	Thr	Tyr	Arg	Leu
		35					40					45			
Ser	Asp	Tyr	Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp
	50					55					60				
Cys	Ser	Ile	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Thr	Asp	Glu	Ile	Ala	Lys
65				70						75					80
Glu	Ala	Gly	Asp	Asp	Tyr	Val	Val	Leu	Thr	Val	Val	Ser	Pro	Gly	His
			85						90					95	
Lys	Gly	Glu	Gln	Ser	Glu	Ala	Asp	Phe	Lys	Asn	Trp	Tyr	Lys	Gly	Leu
			100					105						110	
Asp	Tyr	Lys	Asn	Leu	Pro	Val	Leu	Val	Asp	Pro	Ser	Gly	Lys	Leu	Leu
		115					120					125			
Glu	Thr	Tyr	Gly	Val	Arg	Ser	Tyr	Pro	Thr	Gln	Ala	Phe	Ile	Asp	Lys
		130				135					140				
Glu	Gly	Lys	Leu	Val	Lys	Thr	His	Pro	Gly	Phe	Met	Glu	Lys	Asp	Ala
145					150					155					160
Ile	Leu	Gln	Thr	Leu	Lys	Glu	Leu	Ala							
				165											

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

09765272.012201

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60  
TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTTTCT GGGGAGTGGA 120  
GGAATATTTC TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180  
AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240  
CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300  
CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360  
TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420  
GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480  
GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540  
TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600  
GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660  
TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720  
GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTTAC 780  
CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840  
TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTGGG CATGTCTTTA CGGATGGTCC 900  
ACAGGACAAG GGCGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA 960  
AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys  
1 5 10 15  
Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala  
20 25 30  
Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly  
35 40 45  
Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr  
50 55 60  
Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val  
65 70 75 80

315

Thr	Tyr	Asp	Ala	Lys	Gln	Ile	Ser	Leu	Lys	Glu	Ile	Leu	Leu	His	Tyr	
				85					90					95		
Phe	Arg	Ile	Ile	Asn	Pro	Thr	Ser	Lys	Asn	Lys	Gln	Gly	Asn	Asp	Val	
			100					105					110			
Gly	Thr	Gln	Tyr	Arg	Thr	Gly	Val	Tyr	Tyr	Thr	Asp	Asp	Lys	Asp	Leu	
		115					120					125				
Glu	Val	Ile	Asn	Gln	Val	Phe	Asp	Glu	Val	Ala	Lys	Lys	Tyr	Asp	Gln	
	130					135					140					
Pro	Leu	Ala	Val	Glu	Lys	Glu	Asn	Leu	Lys	Asn	Phe	Val	Val	Ala	Glu	
145					150					155					160	
Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His	
			165						170					175		
Ile	Asn	Val	Asn	Gln	Ala	Ala	Tyr	Pro	Val	Ile	Asp	Ala	Ser	Lys	Tyr	
			180					185					190			
Pro	Lys	Pro	Ser	Asp	Glu	Glu	Leu	Lys	Lys	Thr	Leu	Ser	Pro	Glu	Glu	
		195					200					205				
Tyr	Ala	Val	Thr	Gln	Glu	Asn	Gln	Thr	Glu	Arg	Ala	Phe	Ser	Asn	Arg	
	210					215					220					
Tyr	Trp	Asp	Lys	Phe	Glu	Ser	Gly	Ile	Tyr	Val	Asp	Ile	Ala	Thr	Gly	
225					230					235					240	
Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp	
			245						250				255			
Pro	Ser	Phe	Thr	Gln	Pro	Ile	Ser	Pro	Asp	Val	Val	Thr	Tyr	Lys	Glu	
			260					265					270			
Asp	Lys	Ser	Tyr	Asn	Met	Thr	Arg	Met	Glu	Val	Arg	Ser	Arg	Val	Gly	
	275					280					285					
Asp	Ser	His	Leu	Gly	His	Val	Phe	Thr	Asp	Gly	Pro	Gln	Asp	Lys	Gly	
	290					295					300					
Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	Leu	Ser	Ile	Arg	Phe	Ile	Pro	Lys	
305					310					315					320	
Asp	Gln	Met	Glu	Glu	Lys	Gly	Thr	Leu	Ile	Tyr						
			325					330								

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 625 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TTGTCAGTCA	GGTTCTAATG	GTTCTCAGTC	TGCTGTGGAT	GCTATCAAAC	AAAAAGGGAA	60
ATTAGTTGTG	GCAACCAAGTC	CTGACTATGC	ACCCTTTGAA	TTTCAATCAT	TGGTTGATGG	120

09765272 1012204

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG 180  
GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAAGTGG 240  
TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300  
TTTTTCAATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360  
AAAATACAAG GATTTAAC TA GCCTAGAAAG TGCTAATATT GCAGCCCAAA AAGGGACTGT 420  
TCCAGAAATCA ATGGTCAAGG AACAAATGCC AAAAGTTCAA TTAAGTTCCC TAACTAATAT 480  
GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTCATA TGGATGAGCC 540  
TGTTCGACTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600  
GATGAAGGAC GGCGACGCCA ATGCC 625

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys Gln Ser Gly Ser Asn Gly Ser Gln Ser Ala Val Asp Ala Ile Lys  
1 5 10 15  
Gln Lys Gly Lys Leu Val Val Ala Thr Ser Pro Asp Tyr Ala Pro Phe  
20 25 30  
Glu Phe Gln Ser Leu Val Asp Gly Lys Asn Gln Val Val Gly Ala Asp  
35 40 45  
Ile Asp Met Ala Gln Ala Ile Ala Asp Glu Leu Gly Val Lys Leu Glu  
50 55 60  
Ile Ser Ser Met Ser Phe Asp Asn Val Leu Thr Ser Leu Gln Thr Gly  
65 70 75 80  
Lys Ala Asp Leu Ala Val Ala Gly Ile Ser Ala Thr Asp Glu Arg Lys  
85 90 95  
Glu Val Phe Asp Phe Ser Ile Pro Tyr Tyr Glu Asn Lys Ile Ser Phe  
100 105 110  
Leu Val Arg Lys Ala Asp Val Glu Lys Tyr Lys Asp Leu Thr Ser Leu  
115 120 125  
Glu Ser Ala Asn Ile Ala Ala Gln Lys Gly Thr Val Pro Glu Ser Met  
130 135 140  
Val Lys Glu Gln Leu Pro Lys Val Gln Leu Thr Ser Leu Thr Asn Met  
145 150 155 160  
Gly Glu Ala Val Asn Glu Leu Gln Ala Gly Lys Ile Asp Ala Val His

0916372 012201  
102210 2259460

165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu  
 180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT 60  
 TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA 120  
 AAATTCCAAT AAATCCCAAG GAGATTATAC GGAATCATT GTGAATAAAA ACACAGAAAA 180  
 TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA 240  
 AAAAGCAATC AAGGAACTAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG 300  
 AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT 360  
 AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG 420  
 AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG 480  
 GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG 540  
 ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA 600  
 CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA 660  
 TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC 720  
 ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA 780  
 CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTG 840  
 TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT 900  
 CAAACACAAC GTTGATGTTG TTTCCGTATC ATCTGGTTTT ACAGGAACAG GTCTTGTAGG 960  
 TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC 1020  
 TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA 1080  
 TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC 1140  
 GGTGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG 1200  
 TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA 1260  
 TGGAACAAAA GCTCCTAGTA AATTAAATTT TGTATATATA GGCAAGGGGC AAGACCAAGA 1320

05652 012201  
 102210 2259466

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380  
 TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA 1440  
 TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500  
 GGATGAAGGT ACTAAAAGTC AAGTGT'TTC AAT'TTCAGGA GATGATGGTG TAAAGCTATG 1560  
 GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620  
 AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA 1680  
 TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA 1740  
 TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800  
 TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860  
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920  
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980  
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040  
 TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100  
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160  
 AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAACCTCA TATGGTTCCA TTTCTCTTAA 2220  
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280  
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340  
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATG TTCCAGAAAT 2400  
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460  
 CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520  
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC 2580  
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTGATG CCTCTAATGG GATTTGCTGG 2640  
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700  
 AACACTGGGA GGTTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760  
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820  
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880  
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940  
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAAG 3000  
 AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

09765273 012301

(ii) MOLECULE TYPE: protein

Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Thr	Ala	Val	Ile	Lys	Glu
1				5					10					15	
Lys	Glu	Val	Val	Ser	Lys	Asn	Pro	Val	Ile	Asp	Asn	Asn	Thr	Ser	Asn
			20					25					30		
Glu	Glu	Ala	Lys	Ile	Lys	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp
		35					40					45			
Tyr	Thr	Asp	Ser	Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu
	50					55					60				
Asp	Lys	Val	Val	Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu
65				70						75					80
Lys	Ala	Ile	Lys	Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr
				85					90					95	
Thr	Tyr	Asp	Arg	Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Thr	Pro	Asp
			100					105					110		
Asn	Leu	Asp	Lys	Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg
		115					120					125			
Ala	Gln	Lys	Val	Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly
	130					135					140				
Val	Glu	Glu	Ala	Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly
145					150					155					160
Lys	Asn	Phe	Asp	Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly
				165					170					175	
Thr	Asp	Tyr	Arg	His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala
			180					185					190		
Ser	Met	Arg	Phe	Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Tyr
		195					200					205			
Trp	Leu	Ser	Asp	Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly
	210					215					220				
Lys	Ile	Thr	Val	Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro
225					230					235					240
His	Gly	Met	His	Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln
				245					250					255	
Asp	Ile	Lys	Asn	Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln
			260					265					270		
Ile	Phe	Ser	Tyr	Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly
		275					280					285			

Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser Ile Lys His Asn Val  
 290 295 300  
 Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly Thr Gly Leu Val Gly  
 305 310 315 320  
 Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro  
 325 330 335  
 Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser Ala Ser Ser Ser Ser  
 340 345 350  
 Trp Asp Leu Val Ala Asn Asn His Leu Lys Met Thr Asp Thr Gly Asn  
 355 360 365  
 Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile Ala Val Ala Ser Ala  
 370 375 380  
 Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser  
 385 390 395 400  
 Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr  
 405 410 415  
 Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr  
 420 425 430  
 Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly  
 435 440 445  
 Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala  
 450 455 460  
 Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn  
 465 470 475 480  
 Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met  
 485 490 495  
 Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser  
 500 505 510  
 Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys  
 515 520 525  
 Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu  
 530 535 540  
 Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn  
 545 550 555 560  
 Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp  
 565 570 575  
 Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser  
 580 585 590  
 Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro  
 595 600 605  
 Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr  
 610 615 620

Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala  
 625 630 635 640  
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro  
 645 650 655  
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu  
 660 665 670  
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr  
 675 680 685  
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly  
 690 695 700  
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala  
 705 710 715 720  
 Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser  
 725 730 735  
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys  
 740 745 750  
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser  
 755 760 765  
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr  
 770 775 780  
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile  
 785 790 795 800  
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr  
 805 810 815  
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn  
 820 825 830  
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His  
 835 840 845  
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys  
 850 855 860  
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly  
 865 870 875 880  
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly  
 885 890 895  
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys  
 900 905 910  
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp  
 915 920 925  
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr  
 930 935 940  
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly  
 945 950 955 960

09523 01304

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile  
995 1000 1005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTGGTCGAA	GTTGAGACTC	CTCAATCAAT	AACAAATCAG	GAGCAAGCTA	GGACAGAAAA	60
CCAAGTAGTA	GAGACAGAGG	AAGCTCCAAA	AGAAGAAGCA	CCTAAAACAG	AAGAAAGTCC	120
AAAGGAAGAA	CCAAAATCGG	AGGTAAAAACC	TACTGACGAC	ACCCTTCCTA	AAGTAGAAGA	180
GGGGAAAGAA	GATTTCAGCAG	AACCAGCTCC	AGTTGAAGAA	GTAGGTGGAG	AAGTTGAGTC	240
AAAACCAGAG	GAAAAAGTAG	CAGTTAAGCC	AGAAAGTCAA	CCATCAGACA	AACCAGCTGA	300
GGAATCAAAA	GTTGAACAAG	CAGGTGAACC	AGTCGCGCCA	AGAGAAGACG	AAAAGGCACC	360
AGTCGAGCCA	GAAAAGCAAC	CAGAAGCTCC	TGAAGAAGAG	AAGGCTGTAG	AGGAAACACC	420
GAAACAAGAA	GAGTCAACTC	CAGATACCAA	GGCTGAAGAA	ACTGTAGAAC	CAAAAGAGGA	480
GACTGTTAAT	CAATCTATTG	AACAACCAAA	AGTTGAAACG	CCTGCTGTAG	AAAAACAAAC	540
AGAACCAACA	GAGGAACCAA	AAGTTGAACA	AGCAGGTGAA	CCAGTCGCGC	CAAGAGAAGA	600
CGAACAGGCA	CCAACGGCAC	CAGTTGAGCC	AGAAAAGCAA	CCAGAAGTTC	CTGAAGAAGA	660
GAAGGCTGTA	GAGGAAACAC	CGAAACCAGA	AGATAAAATA	AAGGGTATTG	GTACTAAAGA	720
ACCAGTTGAT	AAAAGTGAGT	TAAATAATCA	AATTGATAAA	GCTAGTTCAG	TTTCTCCTAC	780
TGATTATTCT	ACAGCAAGTT	ACAATGCTCT	TGGACCTGTT	TTAGAAACTG	CAAAAGGTGT	840
CTATGCTTCA	GAGCCTGTAA	AACAGCCTGA	GGTAAATAGC	GAGACAAATA	AACTTAAAAC	900
GGCTATTGAC	GCTCTAAACG	TTGATAAAAC	TGAATTAAAC	AATACGATTG	CAGATGCAAA	960
AACAAAGGTA	AAAGAACATT	ACAGTGATAG	AAGTTGGCAA	AACCTCCAAA	CTGAAGTTAC	1020
AAAGGCTGAA	AAAGTTGCAG	CTAATACAGA	TGCTAAACAA	AGTGAAGTTA	ACGAAGCTGT	1080
TGAAAAATTA	ACTGCAACTA	TTGAAAAATT	GGTTGAATTA	TCTGAAAAGC	CAATATTAAC	1140
ATTGACTAGT	ACCGATAAGA	AAATATTGGA	ACGTGAAGCT	GTTGCTAAGT	ATACTCTAGA	1200
AAATCAAAAC	AAAAACAAAAA	TCAAATCAAT	CACAGCTGAA	TTGAAAAAAG	GAGAAGAAGT	1260

TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAACTATAA GCGCTGCATT 1320  
 TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG 1380  
 TAACGGTGAA GAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAAGT 1440  
 TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAACTAA 1500  
 TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTTAA AAATAACTTC 1560  
 AAATAATCAG AAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTAACGG 1620  
 AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680  
 TAAATTTGAA GAAGAA 1696

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val Val Glu Val Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala  
 1 5 10 15  
 Arg Thr Glu Asn Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu  
 20 25 30  
 Ala Pro Lys Thr Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val  
 35 40 45  
 Lys Pro Thr Asp Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp  
 50 55 60  
 Ser Ala Glu Pro Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser  
 65 70 75 80  
 Lys Pro Glu Glu Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp  
 85 90 95  
 Lys Pro Ala Glu Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala  
 100 105 110  
 Pro Arg Glu Asp Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu  
 115 120 125  
 Ala Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu  
 130 135 140  
 Ser Thr Pro Asp Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu  
 145 150 155 160  
 Thr Val Asn Gln Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val  
 165 170 175  
 Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly

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324

180

185

190

Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro	Val
		195					200					205			
Glu	Pro	Glu	Lys	Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu
		210				215					220				
Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys	Glu
225					230					235					240
Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser	Ser
			245						250					255	
Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	Ala	Ser	Tyr	Asn	Ala	Leu	Gly	Pro
			260					265					270		
Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	Tyr	Ala	Ser	Glu	Pro	Val	Lys	Gln
		275					280					285			
Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	Lys	Leu	Lys	Thr	Ala	Ile	Asp	Ala
	290					295					300				
Leu	Asn	Val	Asp	Lys	Thr	Glu	Leu	Asn	Asn	Thr	Ile	Ala	Asp	Ala	Lys
305					310					315					320
Thr	Lys	Val	Lys	Glu	His	Tyr	Ser	Asp	Arg	Ser	Trp	Gln	Asn	Leu	Gln
				325					330					335	
Thr	Glu	Val	Thr	Lys	Ala	Glu	Lys	Val	Ala	Ala	Asn	Thr	Asp	Ala	Lys
		340						345					350		
Gln	Ser	Glu	Val	Asn	Glu	Ala	Val	Glu	Lys	Leu	Thr	Ala	Thr	Ile	Glu
		355					360					365			
Lys	Leu	Val	Glu	Leu	Ser	Glu	Lys	Pro	Ile	Leu	Thr	Leu	Thr	Ser	Thr
	370					375					380				
Asp	Lys	Lys	Ile	Leu	Glu	Arg	Glu	Ala	Val	Ala	Lys	Tyr	Thr	Leu	Glu
385					390					395					400
Asn	Gln	Asn	Lys	Thr	Lys	Ile	Lys	Ser	Ile	Thr	Ala	Glu	Leu	Lys	Lys
				405					410					415	
Gly	Glu	Glu	Val	Ile	Asn	Thr	Val	Val	Leu	Thr	Asp	Asp	Lys	Val	Thr
			420					425					430		
Thr	Glu	Thr	Ile	Ser	Ala	Ala	Phe	Lys	Asn	Leu	Glu	Tyr	Tyr	Lys	Glu
		435					440					445			
Tyr	Thr	Leu	Ser	Thr	Thr	Met	Ile	Tyr	Asp	Arg	Gly	Asn	Gly	Glu	Glu
	450					455					460				
Thr	Glu	Thr	Leu	Glu	Asn	Gln	Asn	Ile	Gln	Leu	Asp	Leu	Lys	Lys	Val
465					470					475					480
Glu	Leu	Lys	Asn	Ile	Lys	Arg	Thr	Asp	Leu	Ile	Lys	Tyr	Glu	Asn	Gly
				485					490					495	
Lys	Glu	Thr	Asn	Glu	Ser	Leu	Ile	Thr	Thr	Ile	Pro	Asp	Asp	Lys	Ser
			500					505					510		
Asn	Tyr	Tyr	Leu	Lys	Ile	Thr	Ser	Asn	Asn	Gln	Lys	Thr	Thr	Leu	Leu

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525

Lys Phe Glu Glu Glu  
565

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AACACCTGTA	TATAAAGTTA	CAGCAATCGC	AGACAATTTA	GTCTCTAGAA	CTGCTGATAA	60
TAAATTTGAA	GAAGAATACG	TTCACTATAT	TGAAAAACCT	AAAGTCCACG	AAGATAATGT	120
ATATTATAAT	TTCAAAGAAT	TAGTGGAAGC	TATTCAAAAC	GATCCTTCAA	AAGAATATCG	180
TCTGGGACAA	TCAATGAGCG	CTAGAAATGT	TGTTCCCTAAT	GGAAAAATCAT	ATATCACTAA	240
AGAATTCACA	GGAAAACTTT	TAAGTTCTGA	AGGAAAACAA	TTTGCTATTA	CTGAATTGGA	300
ACATCCATTA	TTTAATGTGA	TAACAAACGC	AACGATAAAT	AATGTGAATT	TTGAAAATGT	360
AGAGATAGAA	CGTTCTGGTC	AAGATAATAT	TGCATCATT	GCCAATACTA	TGAAAGGTTC	420
TTCAGTTATT	ACAAATGTCA	AAATTACAGG	CACACTTTCA	GGTCGTAATA	ATGTTGCTGG	480
ATTTGTAAAT	AATATGAATG	ATGGAACTCG	TATTGAAAAT	GTTGCTTTCT	TTGGCAAAC	540
ACACTCTACA	AGTGGAATG	GCTCTCATAC	AGGGGGAATT	GCAGGTACAA	ACTATAGAGG	600
AATTGTTAGA	AAAGCATATG	TTGATGCTAC	TATTACAGGA	AACAAAACAC	GCGCCAGCTT	660
GTTAGTTCCT	AAAGTAGATT	ATGGATTAAC	TCTAGACCAT	CTTATTGGTA	CAAAAGCTCT	720
CCTAACTGAG	TCGGTTGTAA	AAGGTAAAAT	AGATGTTTCA	AATCCAGTAG	AAGTTGGAGC	780
AATAGCAAGT	AAGACTTGGC	CTGTAGGTAC	GGTAAGTAAT	TCTGTCAGCT	ATGCTAAGAT	840
TATCCGTGGA	GAGGAGTTAT	TCGGCTCTAA	CGACGTTGAT	GATTCTGATT	ATGCTAGTGC	900
TCATATAAAA	GATTTATATG	CGGTAGAGGG	ATATTCGTCA	GGTAATAGAT	CATTTAGGAA	960
ATCTAAAACA	TTTACTAAAT	TAATAAAGA	ACAAGCTGAT	GCTAAAGTTA	CTACTTTCAA	1020
TATTACTGCT	GATAAATTAG	AAAGTGATCT	ATCTCCTCTT	GCAAACTTA	ATGAAGAAAA	1080
AGCCTATTCT	AGTATTCAAG	ATTATAACGC	TGAATATAAC	CAAGCCTATA	AAAATCTTGA	1140
AAAATTAATA	CCATTCTACA	ATAAAGATTA	TATTGTATAT	CAAGGTAATA	AATTAAATAA	1200

AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260  
 TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320  
 TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380  
 TGACTIONAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440  
 TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500  
 AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560  
 CACAGATGTT AAAGAAAACCT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620  
 TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680  
 AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740  
 TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800  
 ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860  
 CGACGCATTC GGTCAAGTA 1879

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile	Ala	Asp	Asn	Leu	Val	Ser	Arg
1				5					10					15	
Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu	Tyr	Val	His	Tyr	Ile	Glu	Lys
			20					25					30		
Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr	Tyr	Asn	Phe	Lys	Glu	Leu	Val
		35					40					45			
Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys	Glu	Tyr	Arg	Leu	Gly	Gln	Ser
	50					55					60				
Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn	Gly	Lys	Ser	Tyr	Ile	Thr	Lys
65				70					75					80	
Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser	Glu	Gly	Lys	Gln	Phe	Ala	Ile
			85					90					95		
Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn	Val	Ile	Thr	Asn	Ala	Thr	Ile
		100						105					110		
Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu	Ile	Glu	Arg	Ser	Gly	Gln	Asp
		115					120					125			
Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met	Lys	Gly	Ser	Ser	Val	Ile	Thr
	130					135					140				

Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly  
 145 150 155 160  
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe  
 165 170 175  
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly  
 180 185 190  
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp  
 195 200 205  
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys  
 210 215 220  
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu  
 225 230 235 240  
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val  
 245 250 255  
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser  
 260 265 270  
 Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly  
 275 280 285  
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp  
 290 295 300  
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys  
 305 310 315 320  
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val  
 325 330 335  
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro  
 340 345 350  
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr  
 355 360 365  
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro  
 370 375 380  
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys  
 385 390 395 400  
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn  
 405 410 415  
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val  
 420 425 430  
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser  
 435 440 445  
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile  
 450 455 460  
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn  
 465 470 475 480

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 102210"2259/60

Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met  
 485 490 495  
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys  
 500 505 510  
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr  
 515 520 525  
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp  
 530 535 540  
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys  
 545 550 555 560  
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val  
 565 570 575  
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp  
 580 585 590  
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly  
 595 600 605  
 Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly  
 610 615 620  
 Gln Val  
 625

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTTT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAAAAATTC	240
TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCTTTGG	360
TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420
TGCAGATGGT TATAGAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTAA	480
ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTTATAACG CTCCTGGTGG	540
ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT	600

CTTTGGTCCT ATGGATAAGT ATTATAATTA TAATGGAACA GGAGCTTATG CTGCTATATA 660  
 TCCTAACTCT GATGATATTA GAACTGATGT AAAATATGTT CATTTAGAAA TGGTTGGTGA 720  
 ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT 780  
 AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA 840  
 AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT 900  
 TAAACGCAAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAACCTC TAAAAACACG 960  
 AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAACCTCTC TTGATGAAAT 1020  
 TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA 1080  
 AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT 1140  
 AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA 1200  
 ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA 1260  
 CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG 1320  
 TAAAGGTGCT CCTGGAGCTG TTTCATTCAA ACATAATGCT TTTAGATTAT GGGGTTACTA 1380  
 CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAC 1440  
 AGATGGTGAG TCTGTTCTAA GTGATGAATA TATTATCAAG AAAATATCTA ACAATACATT 1500  
 TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAAGAA GTTAAAGATA AAGCAACGAA 1560  
 AGGATTAACA ACATTCGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC 1620  
 ATTGTTTAAA GAAGCTGTTA AAAAAGATGC CGAAACTCTT AAACAAGAAG CAAACGGTAA 1680  
 TAAAACAGTA TCTATGAATA ATACAGTTAA ATTAAAAGAA GCTGTTTATA AGAAACTTCT 1740  
 TCAACAAACA AATAGCTTTA AAACCTCAAT CTTTAAA 1777

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu	Asp	Arg	Leu	Ile	Glu	Ile	Gly	Ser	Lys	Glu	Asn	Asn	Ile	Lys	Gly
1				5					10					15	
Ser	Arg	Thr	Phe	Asp	Ala	Phe	Gly	Gln	Val	Leu	Ala	Lys	Tyr	Thr	Lys
			20					25					30		
Ser	Gly	Asn	Leu	Asp	Ala	Phe	Leu	Asn	Tyr	Asn	Arg	Gln	Leu	Phe	Thr
		35					40					45			
Asn	Ile	Asp	Asn	Met	Asn	Asp	Trp	Phe	Ile	Asp	Ala	Thr	Glu	Asp	His

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50

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60

Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser  
 65 70 75 80  
 Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr  
 85 90 95  
 Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser  
 100 105 110  
 Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys  
 115 120 125  
 Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr  
 130 135 140  
 Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys  
 145 150 155 160  
 Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn  
 165 170 175  
 Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys  
 180 185 190  
 Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr  
 195 200 205  
 Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp  
 210 215 220  
 Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu  
 225 230 235 240  
 Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg  
 245 250 255  
 Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu  
 260 265 270  
 Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe  
 275 280 285  
 Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn  
 290 295 300  
 Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg  
 305 310 315 320  
 Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu  
 325 330 335  
 Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp  
 340 345 350  
 Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn  
 355 360 365  
 Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu  
 370 375 380  
 Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln

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385		390		395		400
Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala						
	405			410		415
Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr						
	420			425		430
Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser						
	435			440		445
Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn						
	450			455		460
Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr						
	465			470		475
Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser						
	485			490		495
Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys						
	500			505		510
Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn						
	515			520		525
Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu						
	530			535		540
Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn						
	545			550		555
Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr						
	565			570		575
Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys						
	580			585		590

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGGCGCA	120
GAAAAAGGTT GGAGCGCAGA AAGGTTTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180
AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAAATCAGG	240
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC	300
TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC	360
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA	420

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr  
 1 5 10 15  
 Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr  
 20 25 30  
 Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly  
 35 40 45  
 Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu  
 50 55 60  
 Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly  
 65 70 75 80  
 Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val  
 85 90 95  
 Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu  
 100 105 110  
 Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu  
 115 120 125  
 Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu  
 130 135 140  
 Leu Asp Lys Leu Ile Glu Glu Ala Leu  
 145 150

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC 60  
 AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT 120  
 CGAAGTTTTA AAGGCAGTAG ATGAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC 180

096532 01224  
 102210 225360

CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240  
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300  
 TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360  
 TAAAACAACA CAAGAGGATA CCGGAACCTC TAACGCTCAA TTCATCAATA ACTGGAATCA 420  
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480  
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540  
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600  
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660  
 GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAACTC AGCAATACCT ATCTAGGTGG 720  
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys	Glu	Asn	Gln	Ala	Thr	Pro	Lys	Glu	Thr	Ser	Ala	Gln	Lys	Thr	Ile	1	5	10	15
Val	Leu	Ala	Thr	Ala	Gly	Asp	Val	Pro	Pro	Phe	Asp	Tyr	Glu	Asp	Lys	20	25	30	
Gly	Asn	Leu	Thr	Gly	Phe	Asp	Ile	Glu	Val	Leu	Lys	Ala	Val	Asp	Glu	35	40	45	
Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Gln	Phe	Gln	Arg	Thr	Ala	Trp	Glu	Ser	50	55	60	
Ile	Phe	Pro	Gly	Leu	Asp	Ser	Gly	His	Tyr	Gln	Ala	Ala	Ala	Asn	Asn	65	70	75	80
Leu	Ser	Tyr	Thr	Lys	Glu	Arg	Ala	Glu	Lys	Tyr	Leu	Tyr	Ser	Leu	Pro	85	90	95	
Ile	Ser	Asn	Asn	Pro	Leu	Val	Leu	Val	Ser	Asn	Lys	Lys	Asn	Pro	Leu	100	105	110	
Thr	Ser	Leu	Asp	Gln	Ile	Ala	Gly	Lys	Thr	Thr	Gln	Glu	Asp	Thr	Gly	115	120	125	
Thr	Ser	Asn	Ala	Gln	Phe	Ile	Asn	Asn	Trp	Asn	Gln	Lys	His	Thr	Asp	130	135	140	
Asn	Pro	Ala	Thr	Ile	Asn	Phe	Ser	Gly	Glu	Asp	Ile	Gly	Lys	Arg	Ile	145	150	155	160

Leu Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val  
 165 170 175

Ser Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val  
 180 185 190

Asp Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser  
 195 200 205

Asp Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu  
 210 215 220

Tyr Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly  
 225 230 235 240

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln  
 245 250

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

09765272 012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCTGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

32

45

33

35

32

(2) INFORMATION FOR SEQ ID NO: 239:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTCAAGATCT CTCCAACATAT GGTAATCTG CGGATGG

37

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCAGTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

0976527204330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTC

34

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GACTGGATCC TGGCAATTCT GGC GGAAGTA AAGATGC

37

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

36

36

(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

40

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

31

31

(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

38

38

(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

37

37

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

006527 01300

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCACCTGCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272 012304

34

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

36

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

37

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

37

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272 012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTTA AATTGACTAT GCGCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTAT GAACTTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:

097533 0430  
 102210 2259450

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

09765272.042204

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTA CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC\_\_

37

(2) INFORMATION FOR SEQ ID NO: 311:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTTCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

00765273 012204

34

34

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

34

34

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

30

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

31

31

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

29

29

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTT TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTCGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

T02210 2/25/94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTTAATCTTG TCCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCTT CATTTGTCTT TGGGTATTTTC GCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCAGTGCAG TTGCTCGTCT CGAGGTTC

28

(2) INFORMATION FOR SEQ ID NO: 329:

09765272.012301

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

09765272.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

32

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

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(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 35 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

36

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

09539460

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

31

(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

32

(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

42

(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

38

(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

36

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAAAC TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

(2) INFORMATION FOR SEQ ID NO: 365:

09622 01204

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTCTGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGTACCAG CAACAAAGCG AGCAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0965372.013304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

096537 013904

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765373 012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG -

47

(2) INFORMATION FOR SEQ ID NO: 392:

0976537 04304

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09/05/2004 10:22:50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG

40

(2) INFORMATION FOR SEQ ID NO: 406:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTCCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

0965273 012201  
T02210 "2259260

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTTTAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTCGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0976537E 043001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

20250429 10:25:29

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTTT CAATATTTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTTCAGGC AAGTCCGTA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GA CTGGATCC GGAAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GA CTGTCGAC AATCAATCCT TCTTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CA GTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GA CTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AG TCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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